Expanding the biocatalytic toolbox of flavoprotein monooxygenases from Rhodococcus jostii RHA1

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Supplementary information

Table S1: GC conditions for the determination of the conversions and enantioselectivities

The following columns were used for the determination of conversions and enantiomeric excesses of the sulfoxides by GC: A: Alltech GT-A (30 m x 0.25 mm x 0.25 µm), B: Hewlett Packard HP-1 (30m x 0.32 mm x 0.25µm, 12.2 psi N_2), C: Chirasil Dex CB (30 m x 0.25 mm x 0.25 µm, 12 psi N_2)

Substrate	Program	Column	t_R (min) substrate	t_R (min) products
thioanisole	70/5/10/200/2	B	11.4	14.9 (sulfoxide) 15.6 (sulfone)
thioanisole	40/0/10/160/8	A	7.5	14.3 (R); 16.7 (S)
p-tolyl methyl sulfide	70/5/10/200/2	B	11.5	15.1(sulfoxide) 15.9 (sulfone)
p-tolyl methyl sulfide	40/0/10/160/8	A	8.3	15.6 (R); 16.5 (S)
benzyl ethyl sulfide	70/5/10/200/2	B	12.5	14.7 (sulfoxide) 16.9 (sulfone)
benzyl ethyl sulfide	40/0/10/160/8	A	8.8	14.4 (R); 15.5 (S) 19.0 (sulfone)
benzyl phenyl sulfide	100/5/5/200/5	B	21.7	27.3 (sulfoxide)
2-indanone	70/10/3/180/5	B	22.3	32.7
cyclopentadecanone	70/10/3/180/5	B	46.5	50.4
phenylacetone	70/7/5/120/2	B	13.5	14.9 (ester) 10.3 (alcohol)
bicyclohept-2-en-6-one	70/5/5/150/0	B	6.6	13.3 (abnormal; AB) 13.4 (normal; N)
bicyclohept-2-en-6-one	130°C isotherrm	C	9.7 and 9.9	(AB: 1*R*,5*S*): 17.6 (N: 1*R*,5*S*): 18.0 (AB: 1*S*,5*R*): 18.3 (N: 1*S*,5*R*): 18.5

[a] Program: initial T (ºC)/ time (min)/ slope (ºC/min)/T (ºC)/ time (min).

Figure S1: CLUSTAL 2.1 multiple sequence alignment

```
15              ------------------------------------------------------------
STMO            ------------------------------------------------------------
9               ------------------------------------------------------------
14              ------------------------------------------------------------
PAMO            ------------------------------------------------------------
24              ------------------------------------------------------------
CHMO            ------------------------------------------------------------
1               ------------------------------------------------------------
CPMO            ------------------------------------------------------------
11              ------------------------------------------------------------
20              ------------------------------------------------------------
3               ------------------------------------------------------------
4               ------------------------------------------------------------
21              ------------------------------------------------------------
23              ------------------------------------------------------------
ACMO            ------------------------------------------------------------
MEKMO           ------------------------------------------------------------
CPDMO           ------------------------------------------------------------
CDMO            ------------------------------------------------------------
7               ------------------------------------------------------------
2               ------------------------------------------------------------
12              ------------------------------------------------------------
6               ------------------------------------------------------------
19              ------------------------------------------------------------
17              ------------------------------------------------------------
5               ------------------------------------------------------------
10              --------------------------MTETIAAGLAVPSD-------RDAQLYNAIAES 26
8               ------------------------------------------------------------
18              ------------------------MKAAQQVQEAGAATDDRINPDRLTESEIRTAVARA 35
HAPMO           ----------------------------------MSAFNTTLPSLDYDDDTLREHLQGA 25
16              ------------------------------------------------------------
EtaA            ------------------------------------------------------------
13              ------------------------------------------------------------
F               MTQTVQPAAVQTSLTPQERVDLWLASFESALAARDVDRAAGMFAVDSFWRDLVAFTWNLK 60
G               MTATLDAPVDTNIPQPGDIARRWLAGFGATLERGDARGAAQHFLVDGWWRDLLSFTWDLH 60
E               MTTTFSDTDLRTD------AQAWLDGFSRFLAAELAP--TAVFAPQAYWRDVLAFTGDLR 52
D               ------------------------------------------------------------
grogan          ------------------------------------------------------------
FMO1Ara         ------------------------------------------------------------
FMO2Ara         ------------------------------------------------------------
FMO1dog         ------------------------------------------------------------
FMO1hum         ------------------------------------------------------------
FMO2hum         ------------------------------------------------------------
FMO3hum         ------------------------------------------------------------
FMO5hum         ------------------------------------------------------------
FMO4hum         ------------------------------------------------------------
FMOFish         ------------------------------------------------------------
FMO1Dro         ------------------------------------------------------------
FMO2Dro         ------------------------------------------------------------
FMOTyr          ------------------------------------------------------------
H               ------------------------------------------------------------
IucD_Lys        ------------------------------------------------------------
PVDA_Orn        ------------------------------------------------------------
SidA_Orn        ------------------------------------------------------------
NRho_Orn        ------------------------------------------------------------
FMOMeth         ------------------------------------------------------------
A               ------------------------------------------------------------
C               ------------------------------------------------------------
B               ------------------------------------------------------------


15              ------------------------------------------------------------
STMO            ------------------------------------------------------------
9               ------------------------------------------------------------
14              ------------------------------------------------------------
PAMO            ------------------------------------------------------------
24              ------------------------------------------------------------
CHMO            ------------------------------------------------------------
1               ------------------------------------------------------------
CPMO            ------------------------------------------------------------
11              ------------------------------------------------------------
20              ------------------------------------------------------------
3               ------------------------------------------------------------
4               ------------------------------------------------------------
21              ------------------------------------------------------------
23              ------------------------------------------------------------
ACMO            ------------------------------------------------------------
MEKMO           ------------------------------------------------------------
```

```
CPDMO           ------------------------------------------------MSQLIQE 7
CDMO            ---------------------------------------------------------
7               ---------------------------------------------------------
2               ---------------------------------------------------------
12              ---------------------------------------------------------
6               ---------------------------------------------------------
19              ---------------------------------------------------------
17              ---------------------------------------------------------
5               ---------------------------------------------------------
10              DPAPLLMALVHATGDTGLLDEFGARLTIEEPGNHYRTGIRPTAPPGIYPEDVAEDIRIRA 86
8               ------------------------------------------------MITEIRKRA 9
18              NVPSLLMVVFQTTGDEKWLAAPYRPTRGKGLGDHDSGGLEEP------IQDEIREAAVKA 89
HAPMO           DIPTLLLTVAHLTGDLQILKPNWKPSIAMGVARSG---------MDLETEAQVREFCLQR 76
16              ---------------------------------------------------------
EtaA            ---------------------------------------------------------
13              ---------------------------------------------------------
F               TVEGRDAVAAMLHARLDDTDPVNFRTT-----ETPDEADG--VTSAWIEFETATGRGKGH 113
G               TTHGRADIESRLADSVPVHEPRHLVLSPAHPAEAVADPEGD-WIQAFFTFETTLARSRGF 119
E               TFS--DEIPAELLRRQELTKATNIRIAEDRTPPRLVERAGIPCLEVIFEFDTLAGSAVGV 110
D               ---------------------------------------------------------
grogan          ---------------------------------------------------------
FMO1Ara         ---------------------------------------------------------
FMO2Ara         ---------------------------------------------------------
FMO1dog         ---------------------------------------------------------
FMO1hum         ---------------------------------------------------------
FMO2hum         ---------------------------------------------------------
FMO3hum         ---------------------------------------------------------
FMO5hum         ---------------------------------------------------------
FMO4hum         ---------------------------------------------------------
FMOFish         ---------------------------------------------------------
FMO1Dro         ---------------------------------------------------------
FMO2Dro         ---------------------------------------------------------
FMOTyr          ---------------------------------------------------------
H               ---------------------------------------------------------
IucD_Lys        ---------------------------------------------------------
PVDA_Orn        ---------------------------------------------------------
SidA_Orn        ---------------------------------------------------------
NRho_Orn        ---------------------------------------------------------
FMOMeth         ---------------------------------------------------------
A               ---------------------------------------------------------
C               ---------------------------------------------------------
B               ---------------------------------------------------------


15              ------------------------------------------------MSARTEVDARANR 13
STMO            ----------------------------------------------MNGQHPRSVVTAPDAT 16
9               ------------------------------------------------------MTVQDN- 6
14              ----------------------------------------------------MSKTISAD--- 8
PAMO            ----------------------------------------------------MAGQTTVDSRR 11
24              ------------------------------------------MTTSMKAANPMNFPSTS 17
CHMO            ------------------------------------------------------MSQKMD----- 6
1               ----------------------------------------------------MSTAAP---- 6
CPMO            ----------------------------------------------MTTMTTMTTEQLGMNN 16
11              ---------------------------------------------MTTASIDTRELD--- 12
20              ----------------------------------------------MTASQADTATRTGKH 15
3               ------------------------------------------------------MNTTLL---- 6
4               ---------------------------------------------MTAIHAPKNDLAQS- 14
21              ----------------------------------------------MSTTASAPTETSAT 14
23              ----------------------------------------------MSTTASAPTETSAT 14
ACMO            ----------------------------------------------MSTTT--------- 5
MEKMO           ----------------------------------------------MSAQSKLAAGSCAY 14
CPDMO           PAEAGVTSQKVSFDHVALREKYRQERDKRLRQDGQEQYLEVAVTCDEYLKDPYADPIVRD 67
CDMO            --------MTTSIDREALRRKYAEERDKRIRPDGNDQYIRLDH-VDGWSHDPYMPITPRE 51
7               ---------------------------------------------MVSYMSLPVTDTSAPP 16
2               ------------------------------------------------MNLP-------- 4
12              ------------------------------------------MVRSAIPVELPVDSVDHPP 19
6               ---------------------------------------------------------
19              ---------------------------------------------MTATTTQHAAAPDGG 15
17              ------------------------------------------------------------MT 2
5               ------------------------------------------------------------MG 2
10              REILTPDVVAELGVPDDELFVRMATVCTSQRVDAEFAPILLEQAGFTKNRRHVPVTVAP- 145
8               REVLTNDLTAVLGVPDPELFRRMASLRTAGTVAEEFVPILLEQAGFQIGQRRVPVTKKP- 68
18              ILDLQNGALPAVETPSPELTVRMISVCTGEEVGEEYGPMLSLELARRAAPDAPSLALEPV 149
HAPMO           LIDFRDSGQPAPGRPTSDQLHILGTWLMGPVIEPYLPLIAEEAVTAEEDLRAPRWHKDHV 136
16              ------------------------------------MSHTETAAETTG---------AK 14
EtaA            ---------------------------------------------------------
13              ----------------------------------MKHITTSHDSDQETPVTITTIPE 23
F               LRLKGDE-----AWTFLTTMQELKGHEERRGRNRVKGAVHGSGGDTLSWAEKREIEEREL 168
G               VRLRRDDDGEWRAWTLISAMEEIKGHEEKKGHRRVQGTNHGAHRGKINWLDRR-TAKGEF 178
E               ARLVDVPERGLLVRSLFTTLDQLADHPERTGEHRPVGQADSSKFGGPNWLDRR-IAAQAY 169
D               ---------------------------------------------------------
```

```
grogan          ------------------------------------------------------------
FMO1Ara         ----------------------------------------------------------MASNY 5
FMO2Ara         ----------------------------------------------------------MAYNY 5
FMO1dog         ------------------------------------------------------------
FMO1hum         ------------------------------------------------------------
FMO2hum         ------------------------------------------------------------
FMO3hum         ------------------------------------------------------------
FMO5hum         ------------------------------------------------------------
FMO4hum         ------------------------------------------------------------
FMOFish         ------------------------------------------------------------
FMO1Dro         ----------------------------------------------------------MMS 3
FMO2Dro         ----------------------------------------------------------MIK 3
FMOTyr          -------MGYRTYAILLCFFNWLHGGDTFPQETTTPVMLDCERVTIRLEAPAPLKAVLLP 53
H               ------------------------------------------------------------
IucD_Lys        ------------------------------------------------------------
PVDA_Orn        ----------------------------------------------------------MTQAT 5
SidA_Orn        --------------------------MESVERKSESSYLGMRNMQPEQRLSLDPPRLRST 34
NRho_Orn        ------------------------------------------------MSESPETVGT 10
FMOMeth         ------------------------------------------------------------
A               ------------------------------------------------------------
C               ------------------------------------------------------------
B               ------------------------------------------------------------

15              IG--DVDAVVVGAGFAGLYAVHKLR-SL-G------------LTVQGVEAAGGVGGTWFW 57
STMO            TGTTSYDVVVVGAGIAGLYAIHRFR-SQ-G------------LTVRAFEAASGVGGVWYW 62
9               ----DFDAVVVGAGISGLYAVYKLR-QR-G------------MRVHGFESAEGVGGTWYH 48
14              -----VDVVVVGAGFAGLYALRKLRDTM-K------------LSTRVFEAGSEVGGTWFW 50
PAMO            QPPEEVDVLVVGAGFSGLYALYRLR-EL-G------------RSVHVIETAGDVGGVWYW 57
24              DTG-IVDVLGVGAGFSGLYLSHRLT-TA-G------------WTFAGFEAGPSVGGTWFW 62
CHMO            -----FDAIVIGGGFGGLYAVKKLRDEL-E------------LKVQAFDKATDVAGTWYW 48
1               AVTEVLDVLVVGAGFAGLYQLENLR-SR-G------------YSVKVVEAGEGLGGIWHW 52
CPMO            SVNDKLDVLLIGAGFTGLYQLYHLR-KL-G------------YKVHLVDAGADIGGIWHW 62
11              EANGVLDVLVVGGGFAGLYQLDQLR-SR-G------------FSVKVVEAGDSLGGIWYW 58
20              SNNDVLDVLIIGGGFSGLYALDRIR-DL-G------------FTAKVWDAAGGLGGIWWW 61
3               ---EELDVLVIGGGFSGVYQLDRLR-TL-G------------YNVKIYEAGTGLGGVWHW 49
4               AETPTYDVIVVGGGFGGIYQLRHLR-DR-G------------FSVILLEASGGFGGAWSL 60
21              -ESLELDALIIGAGVAGLYQLHQLR-EQ-G------------LRVRAYDTAGDVGGTWYW 59
23              -ESLELDALIIGAGVAGLYQLHQLR-EQ-G------------LRVRAYDTAGDVGGTWYW 59
ACMO            -----LDAAVIGTGVAGLYELHMLR-EQ-G------------LEVRAYDKASGVGGTWYW 46
MEKMO           GNVTSLDAMVIGAGVAGLYQLYRLR-EM-G------------LTVRAYDTASGVGGTWYW 60
CPDMO           PVVRETDVFIIGGGFGGLLAAVRLQQAG-V------------SDYVMVERAGDYGGTWYW 114
CDMO            PKLDHVTFAFIGGGFSGLVTAARLRESG-V------------ESVRIIDKAGDFGGVWYW 98
7               AGVRHIDTLIIGSGFAGLGAAIKLTQAG-K------------TDFLVLERGSDVGGTWRD 63
2               ---QHVHTLIVGAGFAGMGLAARILQTQPQ------------ADVLIIERGDDVGGTWRD 49
12              ---EVVDVLVVGAGFGGLGTAIRLKQAG-I------------DDFVVLDRAEDIGGTWRV 63
6               --MTHYDILIVGAGISGIGAAIRLKQSG-I------------DNFAILEKGDALGGTWRD 45
19              GDERHLRVVVVGAGLSGIAAAVKLERAG-I------------TDFVVLEKSDRVGGVWRE 62
17              TGTTEPDVLVVGTGFAGLCMAIKLKEAG-E------------ENVVVLEKADRVGGTWRE 49
5               GEVHRCRVLVIGTGFSGLGTAIQLRRRG-R------------DDFILLEKAREVGGTWRE 49
10              --PADFDVIVIGAGIVGINAGIKLGEAG--------------FRYTIIEEREDVGGTWYR 189
8               --PADLGVIVIGAGMIGLNAAIKLGEAG--------------FGYRVFESRDDIGGTWSR 112
18              DAPEGYSVVVIGTGVAGIAAAQQLEDMG--------------IDYVILEKQPEAGGNWWQ 195
HAPMO           ASGRDFKVVIIGAGESGMIAALRFKQAG--------------VPFVIYEKGNDVGGTWRE 182
16              TPVEHVDVLIIGAGLSGIGAAYHLQDNFPR------------RTYAILESRESIGGTWDL 62
EtaA            -MTEHLDVVIVGAGISGVSAAWHLQDRCPT------------KSYAILEKRESMGGTWDL 47
13              VETMDFDVLIIGAGISGIGAAYHLKTRRPD------------TTFAILEGKDAIGGTWTQ 71
F               GYTRQPYVLVIGGGQGGIALGARLRQLGVP--------------AIVVDKNERPGDQWRN 214
G               -ETEQPAVVIVGAGQGGLALAARLGQLGVD--------------TLLVERNDRIGDSWRK 223
E               -ENRDPDVLIVGGGQSGLTLAARLGQLDVD--------------ALVVDTHARPGDNWRT 214
D               -MNSEVDVAVIGAGQAGLSAAYYLRRFGVEP-----------ESGFVVLDHAPGPGGAWQF 49
grogan          -MDS-VDVVVIGGGQSGLSAGYFLRRSGLS--------------YVILDAEASPGGAWQH 44
FMO1Ara         DKLTSSRVAIIGAGVSGLAAAKNLVHH----------------NPTVFEASDSVGGVWRS 49
FMO2Ara         NMHTSSRVAIIGAGVSGLAAAKHLARH----------------HPQVFEASDSIGGVWRK 49
FMO1dog         ---MAKRVAIVGAGVSGLASIKCCLEEG--------------LEPTCFERSDDLGGLWRF 43
FMO1hum         ---MAKRVAIVGAGVSGLASIKCCLEEG--------------LEPTCFERSDDLGGLWRF 43
FMO2hum         ---MAKKVAVIGAGVSGLISLKCCVDEG--------------LEPTCFERTEDIGGVWRF 43
FMO3hum         ---MGKKVAIIGAGVSGLASIRSCLEEG--------------LEPTCFEKSNDIGGLWKF 43
FMO5hum         --MTKKRIAVIGGGVSGLSSIKCCVEEG--------------LEPVCFERTDDIGGLWRF 44
FMO4hum         ---MAKKVAVIGAGVSGLSSIKCCVDED--------------LEPTCFERSDDIGGLWKF 43
FMOFish         ---MVRTVAVIGAGPSGLTSIKSCLDEG--------------LEPTCFESSDDIGGLWKF 43
FMO1Dro         -------VCIIGAGTAGLCCARHSIANG--------------FETTVFELSDRIGGTWVY 42
FMO2Dro         TSVDKRRVCVIGAGTAGLCALKNSLEAG--------------LDAVAYERGTEIGGTWIF 49
FMOTyr          QASLTPRVCIIGAGYSGLATARHMIDYG--------------LNLTVFEASSYIGGTWKY 99
H               -MLEHLDLVGIGAGPSNLSVAALSAPVG--------------RLRCKFLDRQPTQRWYPGL 46
IucD_Lys        -MKKSVDFIGVGTGPFNLSIAALSHQIG--------------ELDCLFFDEHPHFSWHPGM 46
PVDA_Orn        ATAVVHDLIGVGFGPSNIALAIALQER---------AQAQGALEVLFLDKQGDYRWHGNT 56
SidA_Orn        PQDELHDLLCVGFGPASLAIAIALHDALDPRLNKSASNIHAQPKICFLERQKQFAWHSGM 94
NRho_Orn        DLP-VRDVVGVGFGPANLALAIAIEEHN------AECPPRERISAQFFEKQDRFGWHPGM 63
FMOMeth         ---MATRIAILGAGPSGMAQLRAFQSAQEKG---------AEIPELVCFEKQADWGGQWNY 49
A               --MSEHQVAIVGAGTSGVAAAVALADRG--------------INPLLIDRADQVGSSWHS 44
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C               MSTERFETIVIGAGQAGLATGYHLTRCG--------------QRFVILDAHDRVGDVWRE 46
B               -MTEQHTVVVIGGGQAGLSISWHLVQRG--------------IDHVVLER-ESIAHEWRD 44
                          :* *  .:                          :

15              NRYPGAR--------CDVESVDYSYSFSRELEQEWDWSEKYAT-------QPEILAYINH 102
STMO            NRYPGAR--------CDVESIDYSYSFSPELEQEWNWSEKYAT-------QPEILAYLEH 107
9               NRYPGAR--------CDVESIDYSYSFDEELQQEWTWTERFAT-------QDEILRYLEH 93
14              NRYPGAR--------CDIESVHYSYSFDEDLQQEWQWSERFAG-------QPEILRYLEH 95
PAMO            NRYPGAR--------CDIESIEYCYSFSEEVLQEWNWTERYAS-------QPEILRYINF 102
24              NTYPGAR--------CDVESIYYSYSFDEALQQEWTWSQRFAP-------QAEILSYINH 107
CHMO            NRYPGAL--------TDTETHLYCYSWDKELLQSLEIKKKYVQ-------GPDVRKYLQQ 93
1               NRYPGAR--------VDSEGPIYQFTR-PDLWDEFAFSELYPG-------GDELRRYFKY 96
CPMO            NCYPGAR--------VDTHCQIYQYSI-PELWQEFNWKELFPN-------WAQMREYFHF 106
11              NCYPGAR--------TDSTGQIYQYSR-EDLWKDWSYDELYPS-------WSGVRDYFAY 102
20              NCYPGAR--------TDSTGQIYQFSH-KDLWKKYDFAELYPG-------HDGVRNYFEY 105
3               NSYPGAR--------VDTWAPVYQFSR-EELWRDWNWSEMYPG-------RDELVRYFEY 93
4               NRYPGAR--------VDSHAPVYQFTD-EYLWKDWDFSQMYPD-------HEEMRSYFNY 104
21              NRYPGAR--------FDSEAYIYQYLFSEELYKNWSWSQRFPG-------QPEIERWMHY 104
23              NRYPGAR--------FDSEAYIYQYLFSEELYKNWSWSQRFPG-------QPEIERWMHY 104
ACMO            NRYPGAR--------FDSEAYIYQYLFDEDLYKGWSWSQRFPG-------QEEIERWLNY 91
MEKMO           NRYPGAR--------FDSQAEIYQYWFSEELYKSWQPTERFPA-------QPETEEWLNF 105
CPDMO           NRYPGAQ--------CDIESYVYMPLLEEMGYIP---TEKYAF-------GTEILEYSRS 156
CDMO            NRYPGAM--------CDTAAMVYMPLLEETGYMP---TEKYAH-------GPEILEHCQR 140
7               NTYPGAA--------CDVPS----HLYSYSFALNPEWTRSFST-------QPEIQKYIQS 104
2               NTYPGCA--------CDVPT----SLYSYSFAPSADWSHTFAR-------QPEIHRYLKK 90
12              NTYPGAQ--------CDIPS----ILYSFSFAPNPNWTRLYPL-------QQEIHDYLRS 104
6               NTYPGCA--------CDVPS----ALYSYSFAPNREWSRLFAG-------QDEIRRYIER 86
19              NTYPGCG--------VDIPA----PVYSFSFHPNPRWRSNFAL-------QPELLSYIED 103
17              NTYPGCG--------CDVMS----LMYSFSFAPNRKWTRMYAR-------QPEILDYIER 90
5               NTYPGCA--------CDVPS----HLYSFSFEPNPDWTRMWSG-------QEEIFDYLRG 90
10              NTYPGAA--------VDTPS----HYYSYSFELNPNWSKYYPT-------GPEYQNYLLD 230
8               NVYPGAA--------VDTPS----HYYSYSFELNPDWSRYYPT-------GPEYLDYMHA 153
18              NTYPGAG--------VDTPS----HLYSFSFAKN-DWTTHFEL-------RNELQAYFGA 235
HAPMO           NTYPGCR--------VDINS----FWYSFSFARG-IWDDCFAP-------APQVFAYMQA 222
16              FRYPGIR--------SDSDMYTLGYRF-----KPWSGEKSIAD-------GPSILEYVKD 102
EtaA            FRYPGIR--------SDSDMYTLGFRF-----RPWTGRQAIAD-------GKPILEYVKS 87
13              FRYPGIR--------SDSDMPTFGFGF-----KPWTHKKAIAD-------AHIILDYLQE 111
F               RYKSLCL--------HDPVWYDHLPYMPFPDNWPVFAP------------KDKIGDWLEM 254
G               RYHSLVL--------HDPVWYDHLPYLNFPDHWPVFTP------------KDKLANWFEF 263
E               RYHALTL--------HNAVWLNDLPYMPFPATWPQFVP------------KDKLAGWFEA 254
D               RWPSLTL--------STVNGVHDLPGLGFADTIGVDPNDPEAALVHA---ASAVPQYFAT 98
grogan          AWHSLHL--------FSPAGWSSIPGWPMPASQGPYP---------A---RAEVLAYLAQ 84
FMO1Ara         ---------------CTYETTKLQSARVDYEFSDFPWPNNRDDTTFPP--YLEILDYLES 92
FMO2Ara         ---------------CTYETTKLQSVRVSYELSDFLWPN-RGESSFPT--YVDVLDYLEA 91
FMO1dog         TEHVEEG------RASLYKSVVSNSCKEMSCYSDFPFPED-YPNYVP---NSQFLEYLKM 93
FMO1hum         TEHVEEG------RASLYKSVVSNSCKEMSCYSDFPFPED-YPNYVP---NSQFLEYLKM 93
FMO2hum         KENVEDG------RASIYQSVVTNTSKEMSCFSDFPMPED-FPNFLH---NSKLLEYFRI 93
FMO3hum         SDHAEEG------RASIYKSVFSNSSKEMMCFPDFPFPDD-FPNFMH---NSKIQEYIIA 93
FMO5hum         QENPEEG------RASIYKSVIINTSKEMMCFSDYPIPDH-YPNFMH---NAQVLEYFRM 94
FMO4hum         TESSKDG------MTRVYKSLVTNVCKEMSCYSDFPFHED-YPNFMN---HEKFWDYLQE 93
FMOFish         KEVSEPN------RASIYRSLTINISKEMMCFSDFPIPAD-YPNYMH---HSRILQYFRL 93
FMO1Dro         NEATGAV-NGIDVHSSMYKNLRTNLPKEVMGFPDFEIGAN-EASYVR---SDEICDFLNQ 97
FMO2Dro         SEEMPKD-EYDEVHSSMYEGLRTNLPKEVMGYPDYSYPDDITESFIT---SNQVLEFLRS 105
FMOTyr          TPRVGTDENGAPLFTSAYKNLRTNSFYQTMEFPDYPFPQG-SSSYLS---GPCIYKYLQG 155
H               MLSAAVLQVSHLKDLVTLVDPTSRYTFLNFLARTGRLHRFASLHTPLIA-RREYESYLRW 105
IucD_Lys        LVPDCHMQTVFLKDLVSAVAPTNPYSFVNYLVKHKKFYRFLTSRLRTVS-REEFSDYLRW 105
PVDA_Orn        LVSQSELQISFLKDLVSLRNPTSPYSFVNYLHKHDRLVDFINLGTFYPC-RMEFNDYLRW 115
SidA_Orn        LVPGSKMQISFIKDLATLRDPRSSFTFLNYLHQKGRLIHFTNLSTFLPA-RLEFEDYMRW 153
NRho_Orn        LLDGATMQIAFPKDLVTFRNPRSAFTFFNYLFDQGRLVDFVNHQTFFPT-RHEFHDYLQW 122
FMOMeth         TWRTGLDENGEPVHSSMYRYLWSNGPKECLEFADYTFDEHFGKPIASYPPREVLWDYIKG 109
A               RYDRLRLN----------------TGRQFSHLPNRPYPKGTPTFP----TREQVIEHLER 84
C               RFDSLRL---------YSPARYDGLPGWGIPAPAWSWPG-----------KDEVADYFEA 86
B               SRWDSFT--------LVTPNWQCTLPGYTYSGGDPDGFMNR-----------EQTYQFVRG 86


15              VADRFDLRDRFLFGTRVTSAELDEES-------------------LRWEVRTDRGDV---- 140
STMO            VADRFDLRRDIRFDTRVTSAVLDEEG-------------------LRWTVRTDRGDE---- 145
9               VADRHDLRSAYDFLTRVTSATYDEET-------------------TRWSITTDTGQN---- 131
14              VADRFDLRKDITFDTRVVGVHWDDEN-------------------SVWTVRTDDGAV---- 133
PAMO            VADKFDLRSGITFHTTVTAAAFDEAT-------------------NTWTVDTNHGDR---- 140
24              VADRFDLRKHFTFNTRVVGATWNAAE-------------------RLWEVQLDNGET---- 145
CHMO            VAEKHDLKKSYQFNTAVQSAHYNEAD-------------------ALWEVTTEYGDK---- 131
1               VDAKLDLSKDIYYNTRIISAEFDDTA-------------------NTWTVTAENGSS---- 134
CPMO            ADKKLDLSKDISFNTRVQSAVFDEGT-------------------REWTVRSIGHQP---- 144
11              VDRKLDLSRDIIFSTRVTSADFDGER-------------------NQWTVRTDTGRM---- 140
20              VDSQLDLTRDVVFDTFAESCTWDEET-------------------RQWTARSADGKV---- 143
3               VDEKLDLSKDVRYETRVLAGRFDEET-------------------HRWTLVSRNERTGEEF 135
4               VDSKLDLSKDSRFNTKVVGATFDEEQ-------------------RMWSLETQDGAT---- 142
21              VADTLDLRRDIQLSTMITSAHYDERA-------------------DKWIVRTDRGET---- 142
23              VADTLDLRRDIQLSTMITSAHYDERA-------------------DKWIVRTDRGET---- 142
ACMO            VADSLDLRRDISLETEITSAVFDEDR-------------------NRWTLTTADGDT---- 129
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MEKMO           VANRLNLKKDIQFNTRIASAHFCEDS------------------GRWVVTTAAGET---- 143
CPDMO           IGRKFGLYERTYFQTEVKDLSWDDEA------------------ARWRITTDRGDK---- 194
CDMO            IGKHYDLYDDALFHTEVTDLVWQEHD------------------QRWRISTNRGDH---- 178
7               VADKYKVRNKHLFGCDVQSAHWNEST------------------TRWEVT----TTKG-- 140
2               VAADTGVRSRVVTDCELQEAHWDADE------------------AVWTVR----TSRG-- 126
12              CAENFGIVPHLRMGHDVQDAAWDDDS------------------QVWHVT----TSRG-- 140
6               TAAEHGVPAHVKFGTEMQRAQWSEQS------------------RRWTVD----TSAG-- 122
19              TVDTFGLQSRISMQTDVREAAWSDER------------------RRWILD----TSRG-- 139
17              VVRDYDLAPHIRFGAEVISYEFDETT------------------DRWRVE----TRSGS- 127
5               LADKYDLRRNIHFGRTMTGGHWDAER------------------RRWHVH----TESGD- 127
10              VVEKYRLREHIRFRTRVLSARWLDDE------------------HRWEVVTEDGEGSVV- 271
8               VAEKYDLYKNIELSTAVVTAEWDEAA------------------QKWTVVTRRTDGSTP- 194
18              VLKDLGAGERVRYGTEVRSTRYDEAA------------------AQWSVDMINPDGSSS- 276
HAPMO           VAREHGLYEHIRFNTEVSDAHWDEST------------------QRWQLLYRDSEGQ-T- 262
16              TAAEHGIDRNIRFRHKVVRAEWSTAD------------------SHWTVDAERTDTGETV 144
EtaA            TAAMYGIDRHIRFHHKVISADWSTAE------------------NRWTVHIQSHGT--LS 127
13              TVTENHIDEHIRFGYRVSSAEFSSSA------------------GRWTVTAQRSGSDETV 153
F               YTKVMEIP--YWSSTTCTSATFDDET------------------KEWTVVLDRD-GEDV- 292
G               YADAMELN--VWTGTEFTGGSYDDAT------------------GEWTVTVARDDGSTR- 302
E               YVEAMEIN--FWGTTAFIGGDYDEQS------------------QSWVARVRRGDGTVR- 293
D               YEKQFELP--VHRPVHTRVVCARDE------------------------RLRIETDRG-- 130
grogan          YEQKYALP--VLRPIRVQRVSHFGE------------------------RLRVVARDGR- 117
FMO1Ara         YAKHFDLLKFMKFGSKVIEVRFIGDGETPQMVDLGAYGNLLPGKPVWEVAVQIGDSGDIQ 152
FMO2Ara         YAKHFNLVKFIKFNSKVVELRFIGDGKTLQMGDLGAYGNLLPGKPVWEVAVNTGD-GDIQ 150
FMO1dog         YANRFSLLKCIRFKTKVCKVTKCPD----------------FTVTGQWEVVTQ-HE-GKQE 136
FMO1hum         YANHFDLLKHIQFKTKVCSVTKCSD----------------SAVSGQWEVVTM-HE-EKQE 136
FMO2hum         FAKKFDLLKYIQFQTTVLSVRKCPD----------------FSSSGQWKVVTQ-SN-GKEQ 136
FMO3hum         FAKEKNLLKYIQFKTFVSSVNKHPD----------------FATTGQWDVTTE-RD-GKKE 136
FMO5hum         YAKEFDLLKYIRFKTTVCSVKKQPD----------------FATSGQWEVVTE-SE-GKKE 137
FMO4hum         FAEHFDLLKYIQFKTTVCSITKRPD----------------FSETGQWDVVTE-TE-GKQN 136
FMOFish         YAEHFKLLQHIHFQTSVRSVRQRPD----------------FSHSGQWEVVTENRE-GQEE 137
FMO1Dro         YANHFDLKKHIKFDSYVIRVLQRKT----------------KWQVLFKDLVTN-----KIE 137
FMO2Dro         YAEHFKLKAHIKLQHEVIRVRPRLD----------------DWEVYVWDHSTD-----TCD 145
FMOTyr          YTKQFNLEKHIKFQSLVTSVERVGD----------------MWNVTYMKTDTK-----ENV 195
H               VSDQLD-EVQFGCAVEEVTFDG----------------------QAFRVESTRGT----- 137
IucD_Lys        AAEDMN-NLYFSHTVENIDFDKKR-------------------RLFLVQTSQGE----- 139
PVDA_Orn        VASHFQEQSRYGEEVLRIEPMLS-----------------AGQVEALRVISRNAD-GEEL 157
SidA_Orn        CAQQFSDVVAYGEEVVEVIPGKSDPS---------------SSVVDFFTVRSRNVETGEIS 199
NRho_Orn        AARRVDADVRYGTAVETVRGIRGD-----------------DGVIDRFEVRTADGS----- 161
FMOMeth         RVEKAGVRKYIRFNTAVRHVEFNEDS------------------QTFTVTVQDHTTDTIY 151
A               HARADGIELRLGCPVERLDLTDG----------------------HWRLTTAAGS----- 117
C               YAQRFALPIRTGTTVDGLSRDGDR----------------------YVVTAGTDR----- 119
B               YADTFDPPVREGVAVVAVRQSGSG----------------------GFDVDTTEGP----- 120


15              -LSARYCIFATGAL--STAN--MPNIAGRESFTGDTHHTGQWPH----------EGVDFT 185
STMO            -VSARFLVVAAGPL--SNAN--TPAFDGLDRFTGDIVHTARWPH----------DGVDFT 190
9               -VTARFCVLATGVL--SATN--KPDIPGRDTFGGATYHTGEWPH----------EPVDFA 176
14              -VRSRYFISGAGNL--SVPK--TPEFGGIDNFRGEVLLTGNWPR----------EGADFT 178
PAMO            -IRARYLIMASGQL--SVPQ--LPNFPGLKDFAGNLYHTGNWPH----------EPVDFS 185
24              -RRGRYLISGAGGL--STPK--DFDVPGLGNFTGLQVSTSRWNI----------SLDDLA 190
CHMO            -YTARFLITALGLL--SAPN--LPNIKGINQFKGELHHTSRWP----------DDVSFE 175
1               -FVCKYFVLCTGFA--AKPI--FPKLPGMDSFTGINHHTGLWPE----------GGIEFA 179
CPMO            -IQARFVIANLGFG--ASPS--TPNVDGIETFKGQWYHTALWPQ----------EGVNMA 189
11              -LRARSVVICTGFG--AKPH--IPSINGLNSFAGESHHTALWPQ----------EGLDMA 185
20              -QNARQVIVATGFG--AKPL--YPNLEGLDLFAGDCYHTARWPQ----------EGVDMT 188
3               TTQAQFVIMCLGAG--SKPL--FPNIPGLEKFGGDCFHTARWPL----------EGYDLA 181
4               -FRARFVVFATGST--TEPY--TPSIPDMDAYQGELVHTARWR----------SDLDMT 186
21              -ITTRFLVTCSGML--SAPM--SYVFEGQEEFSGPIFHTSRWPK----------EGADLD 187
23              -ITTRFLVTCSGML--SAPM--SYVFEGQEEFSGPIFHTSRWPK----------EGADLD 187
ACMO            -IDAQFLITCCGML--SAPM--KDLFPGQSDFGGQLVHTARWPK----------EGIDFA 174
MEKMO           -INTQYLISCCGML--SAPL--SDRFPGQADFQGQIYHTGLWPK----------DPVDFN 188
CPDMO           -FSARFVCMSTGPL--QRPK--LPGIPGITSFKGHSFHTSRWDYSYTGGDQTGN-LEGLK 248
CDMO            -FTAQFVGMGTGPL--HVAQ--LPGIPGIESFRGKSFHTSRWDYDYTGGDALGAPMDKLA 233
7               NFVAKVLVSAVGAL--CEPS--LPDIKGIEGFEGEIFHSARWNH-----------DADLT 185
2               TVTADVVVAATGAL--STPS--VPDMPGLETFGGTTFHSATWNH-----------DHDLT 171
12              TWEARILVGAMGPF--SEPA--VPNLPALESFRGAVFHSAAWDH-----------EHDLA 185
6               TFTANAVIAAAGPW--NEPL--VPTVPGLDTFTGEVFHSSRWNH-----------TYDLT 167
19              TIVAQHVIFAAGPI--TEPS--TPAVPGIDRFDGDVFHSARWNH-----------DVDLT 184
17              VYHPRIVVAGPGPL--HKPS--VPDLPGRKSFSGVAFHSAEWDH-----------SVDLT 172
5               EYVAQFVVSGIGAL--HIPN--VPDLPGADTFDGTEFHSARWNH-----------DYDLR 172
10              RHRARAVITAMGML--NAAN--IPEVDGLDSFAGRVVHTAEWDS-----------DLDLS 316
8               RHRASAAITGFGFL--NSPN--KTDIPGLDTFEGTVVHTAEWDP-----------SLDLT 239
18              TLRADVVISAVGVL--NRPK--TPNVPGMDSFTGTSFHSAAWPD-----------DLDLD 321
HAPMO           QVDSNVVVFAVGQL--NRPM--IPAIPGIETFKGPMFHSAQWDH-----------DVDWS 307
16              RLTADFLMSCSGYY--RYDEGYTPEFPGLDRFGGRVVHPQQWPE-----------DLDYE 191
EtaA            ALTCEFLFLCSGYY--NYDEGYSPRFAGSEDFVGPIIHPQHWPE-----------DLDYD 174
13              QITARFLFSGTGYY--NHEAGFTPEFDGIEDFTGQVVHPQHWPE-----------ELDYS 200
F               VLHPKQLVLATGMS--GKPN--VPSFPGQDVFRGEQHHSSRHPG-----------PDAYV 337
G               TLHPRHVVLATGMS--GVPN--IPRIAGADTFEGTIEHSSWFVG-----------GREMQ 347
E               TLRPKHVVIATGVS--GIPY--VPELPGLSQFAGRTLHSSEYDD-----------ANDFA 338
```

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D               VVSARGLINATGTW--ERPF--IPRYPGAESFTGRQVHTKDYSS-----------AQDFA 175
grogan          QWLARAVISATGTW--GEAY--TPEYQGLESFAGIQLHSAHYST-----------PAPFA 162
FMO1Ara         WHAFEFVVVCTGKYGDVPRIPAFPAKKGPEMFQGKVMHSMDYCKLEKEE-----ASTLLS 207
FMO2Ara         WHAFEYVVVCAGKYGDVPRTPTFPVKKGPEIFKGKVLHSMDYSKLQKEK-----ASQLLH 205
FMO1dog         SAIFDAVMVCTGFL--TNPHLPLDCFPGINTFKGQYFHSRQYKHPDI-----------FK 183
FMO1hum         SAIFDAVMVCTGFL--TNPYLPLDSFPGINAFKGQYFHSRQYKHPDI-----------FK 183
FMO2hum         SAVFDAVMVCSGHH--ILPHIPLKSFPGMERFKGQYFHSRQYKHPDG-----------FE 183
FMO3hum         SAVFDAVMVCSGHH--VYPNLPKESFPGLNHFKGKCFHSRDYKEPGV-----------FN 183
FMO5hum         MNVFDGVMVCTGHH--TNAHLPLESFPGIEKFKGQYFHSRDYKNPEG-----------FT 184
FMO4hum         RAVFDAVMVCTGHF--LNPHLPLEAFPGIHKFKGQILHSQEYKIPEG-----------FQ 183
FMOFish         RHMFDSVIVCSGHY--SYPHLPLKDFSGIESFEGKYFHSWDYKGPED-----------LR 184
FMO1Dro         FQYFDKVLVANGHY--HTPNYS--QIPNMERFKGQFLHSHDFRSREV-----------FE 182
FMO2Dro         PVYYDFVYVCNGHY--TEPDLP--EVEGLDLFEGNKMHSHLYRKADK-----------FK 190
FMOTyr          SEECGFVVVANGEY--IAPHIP--YFAKQEDFQGKMPHSHDYRDSED-----------YR 240
H               -YAAQHLSIGVGPR-PYVP-ELATGTLGEDVFHSSDFGYHTDSLA--------------- 179
IucD_Lys        -YFARNICLGTGKQ-PYLP-PCVK-HMTQSCFHASEMNLRRPDLS--------------- 180
PVDA_Orn        VRTTRALVVSPGGT-PRIPQVFRALKGDGRVFHHSQYLEHMAKQPCS-----------SGK 206
SidA_Orn        ARRTRKVVIAIGGT-AKMP---SGLPQDPRIIHSSKYCTTLPALLKD-----------KSK 245
NRho_Orn        TVIARNVVMGAGLR-ERIP---EWANPSARCFHNHQFLFRLGEMP------------APV 205
FMOMeth         SEEFDYVVCCTGHF--STPY--VPEFEGFEKFGGRILHAHDFRD-----------ALEFK 196
A               -VDAAEVVVATGFD--HEPF--VPDWPGRGDWRGALVHSSQYRN-----------PSQYN 161
C               -FEADNVVVASGTW----QSPVVPDLAERLDPRIRQLHSSDYRN-----------PSQLQ 163
B               -MHADHVVVAVGGY----HTPVVPRFAERLPADITQLHSSQYRS-----------AGALP 164
                        *

15              GRRVGIIGTGSSGIQSIPLIAEQ-AEHLYVFQRSANYSVPAGNQAWDDEMRRAIKAGYEE 244
STMO            GKRVGVIGTGSSGIQSIPIIAEQ-AEQLFVFQRSANYSIPAGNVPLDDATRAEQKANYAE 249
9               GKRVGVIGTGSSGIQSIPVIAEE-AAEVFVFQRSPNYSIPAGNRPLTGEYIAEVKANYAE 235
14              GKRVAVIGTGASGIQAIPFIAED-AAELVVFQRTPNFATPLGNGPMDPNELADIKSNYAD 237
PAMO            GQRVGVIGTGSSGIQVSPQIAKQ-AAELFVFQRTPHFAVPARNAPLDPEFLADLKKRYAE 244
24              GKRVAVIGTGSSGVQAIPLIAEV-AEHVTVFQRTPNYVMPARNAELPLERVDSIKDDYPA 249
CHMO            GKRVGVIGTGSTGVQVITAVAPL-AKHLTVFQRSAQYSVPIGNDPLSEEDVKKIKDNYDK 234
1               GKRIAIIGTGASGVQVAQEASKK-AAQLTVFQRTPVQALPMRQRQLTDEDNAKIKFDLAD 238
CPMO            GKRVAIIGTGSSGVQVAQEAALD-AKQVTVYQRTPNLALPMHQKQLSAEDNLRMKPELPA 248
11              GKRVGIIGTGSSGVQVTQEAAAD-AEQITIFQRTPNLALPMRQQQLTGQLKEKLKENLPE 244
20              GRKVVVMGTGSSGVQVVQEAGHV-AEHVTVFQRTPNLAIPMQQRALTHDDNEQFRKGLPE 247
3               GKRVAVIGTGASGVQVIQEASKV-ADHLTVFQRTPNTALPMNQRALGEADNAEMKKTYPE 240
4               GKRVAIIGTGASAVQVVQEAGPV-VENLTVFQRTPNISLPMQQKYLDDEEQAALKNKMPD 245
21              GKRVAVIGVGATGIQVIQTVADK-VEHLKVFIRTPQYALPMKNPTFDESDVAAYKSRFAE 246
23              GKRVAVIGVGATGIQVIQTVADK-VEHLKVFIRTPQYALPMKNPTFDESDVAAYKSRFAE 246
ACMO            GKRVGVIGNGATGIQVIQSIAAD-VDELKVFIRTPQYALPMKNPSYGPDEVAWYKSRFGE 233
MEKMO           GKRVAVVGTGATGIQVIQTIAPT-VGSMTVFVRTPQYVIPMRNPKYSKADWEKWGTQFHQ 247
CPDMO           DKRVAIIGTGATSIQAVPHLAAY-AQELYVIQRTPISVGFRGNKPTDPEWAKSLQ---PG 304
CDMO            DKRVAVIGTGATAVQCVPELAKY-CRELYVVQRTPSAVDERGNHPIDEKWFAQIAT--PG 290
7               GKRVAVIGTGASAIQIVPAIGKK-VSHLDVYQRTAPWILPRADR--EYTKLEHTAFKYLP 242
2               GERVAVIGTGASAVQFVPEIAPV-AEHLTVFQRTPAWVIPRLDR--ELSGSEKRLYRRLP 228
12              GERVAVIGTGASAVQIIPRIQPI-VGSMTVFQRTPTWILPHPDQ--PMTGWPRKLFARVP 242
6               GKRVAVVGTGASAVQFVPAIQPT-VESLHLYQRTAQWVLPKPDH--TLPGVERAILRRVP 224
19              GKRVAVVGTGASAVQFIPEIQPD-VEELYVFQRTPAWVVPRLDF--PFPRIAQWAFARVP 241
17              GKRVAVVGTGASAVQFVPEVAKT-AAHVDVFQRTPHWILPKLDR--PITAGEKAVFKAVP 229
5               GKKVAVIGTGASAVQFVPEIVGD-VAELHLYQRTPPWVIPGLNF--GIPPEARRLFGRVP 229
10              GKRVVVLGTGCTSVQVVANIVDQ-VEALDVVVRSPHWLVPEKAVSGDVTEGEKWALANLP 375
8               GKRVVVVGTGCTAVQIVASIVDD-VATVDAIVRSPHWIVPEKLWSTRYRPGRSGQCGTCR 298
18              GKRVAIVGTGASSMQIAPAIADR-VAHLSIYQRSPQWVAPFEKFRAPIPMELRRLMQTCP 380
HAPMO           GKRVGVIGTGASATQFIPQLAQT-AAELKVFARTTNWLLPTPDLHEKISDSCKWLLAHVP 366
16              GKRVVIIGSGATAVTLAPSMAAD-AAHVTMLQRSPTYIISMPAKDKLANKLRRHLPAKLA 250
EtaA            AKNIVVIGSGATAVTLVPALADSGAKHVTMLQRSPTYIVSQPDRDGIAEKLNRWLPETMA 234
13              GKKVVVIGSGATAATLIPAMAGT-AAHITMLQRSPSYVLSLPAEDAIANTLNKLIGPKRA 259
F               GKRVVVVGANNSAHDICKALFEN-GADVTMLQRSSTHIVKSDSLMDLGLGDLYSERAVAA 396
G               GKKALVVGCCNSGHDIAQELNEQ-GADVTILQRSSTYVMSSKHGIPGLFGGVYEE----G 402
E               GQRVVIIGTGNSAHDVAQDLHAH-GIDVTMVQRSSTTIVSVDPSAAAADASYLTA----- 392
D               GQHVLVVGGGISAVQLLDEISRV-TTTTWVTRRP-------------------------- 208
grogan          GMRVAIIGGGNSGAQILAEVSTV-AETTWITQHE--------------------------- 195
FMO1Ara         GKKVAVIGFKKSAIDLALESALA-----NQGEGGKACTMVVRTTHWGIPHYWVWGLPFFL 262
FMO2Ara         GKKVAVIGFKKSAIDLALESALA-----NQGKEGKTCTMVVRTPHWVIPHYW-------- 252
FMO1dog         DKRVLVIGMGNSGTDIAVE----------TSRLAKKVFLSTTGGAWVMSRVFDSGYPWDM 233
FMO1hum         DKRVLVIGMGNSGTDIAVE----------ASHLAEKVFLSTTGGGWVISRIFDSGYPWDM 233
FMO2hum         GKRILVIGMGNSGSDIAVE----------LSKNAAQVFISTRHGTWVMSRISEDGYPWDS 233
FMO3hum         GKRVLVVGLGNSGCDIATE----------LSRTAEQVMISSRSGSWVMSRVWDNGYPWDM 233
FMO5hum         GKRVIIIGIGNSGGDLAVE----------ISQTAKQVFLSTRRGAWILNRVGDYGYPADV 234
FMO4hum         GKRVLVIGLGNTGGDIAVE----------LSRTAAQVLLSTRTGTWVLGRSSDWGYPYNM 233
FMOFish         GKRVVVIGIGNSGGDIAVE----------SSRVAEQVYLSTRRGAWVIRVMSDNGLPVDM 234
FMO1Dro         GKSVLVIGAGPSGMDLSNI----------ISRTADRVTISHH------------------ 214
FMO2Dro         DARVLIIGAGPSGMDITNH----------VRLAAKQVFLSHH------------------ 222
FMOTyr          GLRVLVVGAGPSAFDLATH----------LINVTSMFIHSHH------------------ 272
H               GRDVVVVGGGQSGAEVVEHLLQRSGRDAVGSLTWASRRIGFQPLDESPFTNEWFHPDYVR 239
IucD_Lys        GKRITVVGGGQSGADLFLNALRGEWGEAA-EINWVSRRNNFNALDEAAFADEYFTPEYIS 239
PVDA_Orn        PMKIAIIGGGQSAAEAFIDLNDS---YPSVQADMILRASALKPADDSPFVNEVFAPKFTD 263
SidA_Orn        PYNIAVLGSGQSAAEIFHDLQKR---YPNSRTTLIMRDSAMRPSDDSPFVNEIFNPERVD 302
NRho_Orn        HHRFVVLGAGQSAAEIVQYLHGN---YPEAEVHSVFSRYGYSPADDSPYANRIFDPEAVD 262
FMOMeth         DKTVLLVGSSYSAEDIGSQCYKYGAKKLISCYRTAPMGYKWPENWDERPNLVRVDTENAY 256
```

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A               GKRVLVVGAGCSGMEIAYDLATGGAAKVWLSARTPPNIMLRQGPGGIPG---------- 210
C               DGPVLVVGCSHSGADIALEASRS--------HRTTICGPVRGEVPFDIEG---------- 205
B               AGEVLVVGNGQSGAQIAEDLHLAGRTVHLVTGGAPRVARFYRGRDCVAWLHDMGTYDVSI 224
                     ::*   :.

15              RRRLSRESGGGSPYNAHPK------SALDVSDEERREAYETRWK-LGGV-LFAKTFPDQT 296
STMO            RRRLSRESGGGSPHRPHPK------SALEVSEEERRAVYEERWK-LGGV-LFSKAFPDQL 301
9               RRRLSRMSGGGTPNSAYPK------GALEVDAEERRRVYDEWWQ-RGGY-LFAKAFPDQT 287
14              VRTAARNHFLGVPFNQVQP------SALAVDAEERRRTFDERWN-AGGFRLFIDSYQDIL 290
PAMO            FREESRNTPGGTHRYQGPK------SALEVSDEELVETLERYWQ-EGGP-DILAAYRDIL 296
24              IREECRHSPGGIPDRPVTD------KAFDVSAEERQRRYEAAYE-RSGFNGVGGEFADLL 302
CHMO            IWDGVWNSALAFGLNESTV------PAMSVSAEERKAVFEKAWQTGGGFRFMFETFGDIA 288
1               RFSRRSASFSGFDFDFIPK------SALGVSDEERITTYERLWE-CG-FEFWLGTYQDVF 290
CPMO            AFERRGKCFAGFDFDFIAK------NATELSAAERTEILEELWN-AGGFRYWLANFQDYL 301
11              RFAQRRRSFAGFDMDFIPK------SVFEVSDEERADTYERMWA-TGGFELWLANYQDIL 297
20              RFEARYKAFAGFDFDFLPQ------NAADLSMEERDAIYEKMWA-EGGFEMWLGNFQDIL 300
3               RFANRKNTWAGFDYDFLKE------NIQDLTEERRNEILEELWT-NGGLQPWLGGFLNVL 293
4               VAAKCRETHAAIDYDFDPR------SGFETPEDERNAVFERLWN-QGGFAFWLGNFSDYL 298
21              LKETLPNTFSGFEYDFEH-------VWADLTPEQRNDVLEEIYE-NGSLKLWLASFGEMF 298
23              LKETLPNTFSGFEYDFEH-------VWADLTPEQRNDVLEEIYE-NGSLKLWLASFGEMF 298
ACMO            LKDTLPHTFTGFEYDFTD-------AWEDLTPEQRRARLEDDYE-NGSLKLWLASFAEIF 285
MEKMO           LKKRVRETFAGFDYDFDAG------PWAEKTPDERQAVLEQLWK-DGSLAMWLASFPEMF 300
CPDMO           WQQARMDNFNAITHGMPVD--------VDLVQDSWTKIFGEIGVFLGSD----------G 346
CDMO            WQKRWLDSFTAIWDGVLTDPSELAIEHEDLVQDGWTALGQRMRAAVGSVPIEQYSPENVQ 350
7               GFQKLCRTGIYWMR-----------------------------------------ESQVVGL 263
2               LVQKAVRGTVYGFR-----------------------------------------EALGGVL 249
12              VAQRLARSGLDLVQ-----------------------------------------EAMVPGF 263
6               GAIRALRRVEYAIM-----------------------------------------ESLGLGF 245
19              AVQRALRRLLDVIL-----------------------------------------RTLTWVM 262
17              GVQKAYRGAIYWSH-----------------------------------------ESLIAGF 250
5               LARRMVRAAVYWTY-----------------------------------------ESLALGF 250
10              FYDRWFRLRSYWFASDNLY-------------------------PLPRIDKEWAATHL 408
8               TSRIGSGSEPTGLPQNNLY-------------------------MMPRIDPEWAATHL 331
18              IYHSWYWIRLFWQFGDKVI-------------------------ESLRVDPEWEHPER 413
HAPMO           HYSLWYRVAMAMPQSVGFL-------------------------EDVMVDVGYPPTEL 399
16              YGLTRLKN-----------------------------------------ASVATAIY 266
EtaA            YTAVRWKN-----------------------------------------VLRQAAVY 250
13              YPIIRRKN-----------------------------------------IMMHRGIF 275
F               GMTTEKADLTFASLPYKIM-------------------------HEFQIPIY 423
G               GPAVQDADLIFASLPYPLL-------------------------AGIHAGAT 429
E               -PTLEDCDLLSMATVYPDL-------------------------YTGSQMIT 418
D               ------------------------------------------------------------
grogan          ------------------------------------------------------------
FMO1Ara         FYSSRASQFLHDRPNQSFL------------------------------------------ 281
FMO2Ara         ------------------------------------------------------------
FMO1dog         VFMTRFQNMFRN------------------------------------------------ 245
FMO1hum         VFMTRFQNMLRN------------------------------------------------ 245
FMO2hum         VFHTRFRSMLRN------------------------------------------------ 245
FMO3hum         LLVTRFGTFLKN------------------------------------------------ 245
FMO5hum         LFSSRLTHFIWK------------------------------------------------ 246
FMO4hum         MVTRRCCSFIAQ------------------------------------------------ 245
FMOFish         KYNTRFVHILFQ------------------------------------------------ 246
FMO1Dro         ------------------------------------------------------------
FMO2Dro         ------------------------------------------------------------
FMOTyr          ------------------------------------------------------------
H               YFHGLSQS---------------------------------------------------- 247
IucD_Lys        GFSGLEED---------------------------------------------------- 247
PVDA_Orn        LIYSREHA---------------------------------------------------- 271
SidA_Orn        KFYSQSAA---------------------------------------------------- 310
NRho_Orn        DLHGAPEA---------------------------------------------------- 270
FMOMeth         FADGSSEK---------------------------------------------------- 264
A               ------------------------------------------------------------
C               ------------------------------------------------------------
B               ADHPGGLGKRENTNHYVTG-----------------------------------------R 244


15              KTEAANA-TAREFAEEKIRLLVDD-PAVADKLIPNDH--PIGTKRIVTDTH-YFETYNRP 351
STMO            TDPAAND-TARAFWEEKIRAVVDD-PAVAELLTPKDH--AIGAKRIVTDSG-YYETYNRD 356
9               ISQAAND-TAREYVEAKIREMVTD-PDIADQLVPTDH--PIGTKRIVTDNG-YFKTFNRG 342
14              FDKKAND-TIADYIRDRIHERVQD-PAKAATLAPTGY--AYGTKRPPLETN-YYEAFNRD 345
PAMO            RDRDANE-RVAEFIRNKIRNTVRD-PEVAERLVPKGY--PFGTKRLILEID-YYEMFNRD 351
24              TDVEANR-TASEFIHDKIREIVED-PATAELLVPRYH--PLGAKRSVFGTD-YYETYNRP 357
CHMO            TNMEANI-EAQNFIKGKIAEIVKD-PAIAQKLMPQD----LYAKRPLCDSG-YYNTFNRD 341
1               VDDDAND-TAYEFWRDRTRARIKD-PVIAEKLAPTKKAYPFGVKRPSLEQT-YYDIFNQD 347
CPMO            FDDKAND-YVYEFWRDKVRARIKD-PKVAEKLAPMKKPHPYGAKRPSLEQW-YYEIFNQN 358
11              LDERANR-IMYDFWRDKVRQRVTD-PVKAEKLAPMDPPHPFGTKRPSLEQN-FYDVVNQE 354
20              VDEDANR-TFYDFWRNKVLERVTD-PKKAAIVAPETPPHPYGVKRPSLEQD-YFDVINQS 357
3               FDKDDND-ILYAFWRDKTRQRITR-PELVELLAPTEPIHPWGVKRVSLEQN-YFESLCRD 350
4               FNDKTNA-LTYEFWKNKIKPQIKD-PVKAELLVPEIAPHPFGAKRPALHQN-YYEVMNQT 355
21              YDEEISE-EISEFVRRKMRARLQD-PHLCDLLIPTD--YGFGTHRVPLETN-YLETYHRP 353
23              YDEEISE-EISEFVRRKMRARLQD-PHLCDLLIPTD--YGFGTHRVPLETN-YLETYHRP 353
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ACMO            SDEQVSE-EVSEFVREKMRARLVD-PELCDLLIPSD--YGFGTHRVPLETN-YLEVYHRD 340
MEKMO           FDEQVNE-VVSQFVRIKMRERLRSRPDLCDLLIPTD--YGFGTHRVPLENN-YLEVYLQS 356
CPDMO           SRAQMVDFQLMEQIRARVDQEVKD-PATAESLKPYYN---IMCKRPGFHDS-YLPSFNKP 401
CDMO            RALEEADDEQMERIRARVDEIVTD-PATAAQLKAWFR---QMCKRPCFHDD-YLPAFNRP 405
7               AKAPVFMKPLQFAAERHLRRQIKD-KALRKKVTPNFQ---IGCKRMLISNN-YYPTLAQD 318
2               AHATGLLPVFEMVAKAHLRRQVRD-PELRRKLTPNFT---IGCKRMLLSND-WLRTLDRP 304
12              VYKPALLKGLAALGRAHLRRQVHD-PELRTKLTPTYA---FGCKRPTFSNS-FYPALAQP 318
6               R-HPWILRVIQQVGKAQLRAQVRD-PKLRKALTPDYT---LGCKRLLLSNT-YYPALTRP 299
19              R-CERTARLLNPIGTRWLARQVPD-PALRAALTPNFT---LGCKRLLLSNT-YLPALTKS 316
17              L-HPRLMTVLESAARGLLRRQVRD-PELRATLTPDYI---IGCKRILVSSN-FYPALQRG 304
5               NGHSRLMRPIESMARKNLNRTVAD-PELRRKLTPSYR---IGCKRILGSDV-YYPALISP 305
10              SASPANDMVLRTAQEYLQTSFTDR-PDLIAKLTPDFR---PYAKRIVKDPG-FFAALNRE 463
8               SVSPVNDLVMQTSLQYLEQTLPDR-PDLREKLTPSIR---PYAKRIVKDPG-FLEALERD 386
18              SVNARNDAHREYFTRYITSQVGDR-TDLLDKVMPDYP---PFGKRILLDNG-WYSTLRKD 468
HAPMO           AVSARNDRLRQDISAWMEPQFADR-PDLREVLIPDSP---VGGKRIVRDNGTWISTLKRD 455
16              QLCQRYPEFMKGRIRQLQEKWLPKGYDIDTHFTPRYN--PWDQRLCLVPNGDLFRAIRND 324
EtaA            SACQKWPRRMRKMFLSLIQRQLPEGYDVRKHFGPHYN--PWDQRLCLVPNGDLFRAIRHG 308
13              KACRRSPKLMRKLLIANARRQLPKNFDVDTHFTPRYN--PWDQRLCMVPNGDLFKAISTG 333
F               QKIAERDRDFYDRLEKAGFKLDFGDDGSGLFMKYLRR---GSGYYIDVGAS-----ELVA 475
G               EAIAEKDAEMLDGLRKAGFKVDFGEDGSGLFMKYLRR---GGGYYIDVGAS-----ELIA 481
E               ATMKELDKDLVAALNRIGFRTDYGEEDTGQQMKFMRR---GGGYYLNVGCS-----DLLI 470
D               PEFRDEPFTP--EIGRAAVALVEDRVRR--GLPPGSV---VSVTGLPVTPA-----IRAA 256
grogan          PAFLADDVDGRVLFERATERWKAQQEGREPDLPPG------GFGDIVMVPP-----VLDA 244
FMO1Ara         RTLFCLLFSLLRAVVSKFIESYVLWKLPLEKYGLKPNHSFEEDYASCQMAIIPENFFEEA 341
FMO2Ara         -----------RATVSKFIESYVLWKLPLEKYGLKPDHAFEEDYASCQMALVPEKFFEEA 301
FMO1dog         --------SLPTPIVTWLMARKMNSWFNHANYGLVPEDRTQLREPVLNDELPGCIITGKV 297
FMO1hum         --------SLPTPIVTWLMERKINNWLNHANYGLIPEDRTQLKEFVLNDELPGRIITGKV 297
FMO2hum         --------VLPRTAVKWMIEQQMNRWFNHENYGLEPQNKYIMKEPVLNDDVPSRLLCGAI 297
FMO3hum         --------NLPTAISDWLYVKQMNARFKHENYGLMPLNGVLRKEPVFNDELPASILCGIV 297
FMO5hum         --------ICGQSLANKYLEKKINQRFDHEMFGLKPKHRALSQHPTLNDDLPNRIISGLV 298
FMO4hum         --------VLPSRFLNWIQERKLNKRFNHEDYGLS-ITKGKKAKFIVNDELPNCILCGAI 296
FMOFish         --------LLPVNWLSWFGEKKLNAMYDHTMYALKPKHRLFSTIPVINDELPNKILTGGV 298
FMO1Dro         ------------------------------------------------LTDIGQHSFFENV 227
FMO2Dro         ------------------------------------------------LSTTPNTAFMGNV 235
FMOTyr          ------------------------------------------------LDAK-LPEVYGNY 284
H               ---RRSQLLDAQQLASDGIS-KGLLESIYRRLYYNDFVDSDRIRTTLLPGRELTGLCRGP 303
IucD_Lys        ---IRHQLLDEQKMTSDGIT-ADSLLTIYRELYHRFEVLRKPRNIRLLPSRSVTTLE--S 301
PVDA_Orn        ---ERERLLREYHNTNYSVVDTDLIERIYGVFYRQKVSGIPRHAFRCMTTVER--ATATA 326
SidA_Orn        ---ERQRSLLADKATNYSVVRLELIEEIYNDMYLQRVKNPDETQWQHRILPERKITRVEH 367
NRho_Orn        ---ERLRLLDVHRSTNYSVVDIELINELYATEYQERVRG--RRRLFMRRASEIIAVDETS 325
FMOMeth         ---------VDAIILCTGYIHHFPFLNDDLRLVTNNRLWPLNLYKGVVWEDNPKFFYIGM 315
A               -----------DFIATPLYHAPVPIADAIARFGRERSIGDLREFGLPIPDEGIFARSARL 259
C               ----RLAHLAVPIMWFMANHVLTERTPVGRKMCTHVR---SGGGPLLRVKR------ADL 252
B               DGGRDIDLRAFALAGMRLYGRLLDVVDGTLRFAPTLESSLDAADAVSESIKDSIDAYIDR 304


15              NVTLVDLKAAPIESITPSGITTADA--DYALDTLVFATGFDAMTGALDR---MRIVGRGG 406
STMO            NVELVDLRSTPIVGMDETGIVTTGA--HYDLDMIVLATGFDAMTGSLDK---LEIVGRGG 411
9               NVTLVNLRRTPITEITEAGVLTTNS--FYGLDMLVFATGFDAMTGSLSR---IDIRGRAG 397
14              SVSVVDVKSTPIDEITPTGVRVGDR--VYEVDTIVLATGFDAMTGPLMA---MDIRGRGG 400
PAMO            NVHLVDTLSAPIETITPRGVRTSER--EYELDSLVLATGFDALTGALFK---IDIRGVGN 406
24              NVSLVSLRDEPIETMTANAIVTSKG--TYEADAVVLAIGFDAFTGPLYG---LGLTGASG 412
CHMO            NVRLEDVKANPIVEITENGVKLENGD-FVELDMLICATGFDAVDGNYVR---MDIQGKNG 397
1               NVRVVDLHEDPIETITPTGLKTTSE--QHEFDIIVYATGFDAVTGGLTA---MDIRGTDG 402
CPMO            NVTLVDVNETPVLRITEKGIVTAEG--EAEFDLIVFATGFDAVTGGLTS---IDFRNNQG 413
11              NVDIVDVNEDPIERITPAGVQTKSG--LHEFDILVFATGFDANRGGITS---IDIRGTND 409
20              NVEVIDSNLTPIRRVLPHGIETDDG--VIECDLLVLATGFDNNSGGIMA---IDITGVDG 412
3               NVELVDTSANPIREVASDAIITADGT-RHEVDVIVLATGFDSVTGGLTA---IDIRGTGN 406
4               NVSLVSTKETPIVGFTETGIRTADGVEHGEFDIIVLATGFNNNTGALTS---IDVQNANG 412
21              NVEAIGVRDNPITRIVPQGLVLADG-TLHEVDVIVMATGFDAGTGSLTR---IDIRGRGG 409
23              NVEAIGVRDNPITRIVPQGLVLADG-TLHEVDVIVMATGFDAGTGSLTR---IDIRGRGG 409
ACMO            NVTAVLVRDNPITRIRENGIELADG-TVHELDVIIMATGFDAGTGALTR---IDIRGRDG 396
MEKMO           NVKAVDCKQSPIERIVPQGIQTADG-KIHEVDIIVLAVGFDAGSGALSR---IDIRGRDS 412
CPDMO           NVTLVDTQGAGVERITEKGLVVNGR--EYEVDCLIYATGFEYQ-TKLSRRNGYEIHGRNG 458
CDMO            NTHLVDTGGKGVERITENGVVVAGV--EYEVDCIVYASGFEFLGTGYTDRAGFDPTGRDG 463
7               NVDLVTDG---IAEVTADSVVSKDG-TVREVDAIVVATGFHVTDSPTFEG----IFGKDG 370
2               DVTLVDAG---LAGVTPDGVVDALG-NEHKVDTIIFATGFTPTEPPVAHA----LRGANG 356
12              NVDVITDG---IREVRSNGIVTEDG-VLHEVDTIVMGTGFRLTDNPAFDV----VRGRDG 370
6               NVEVHANA---VESVRGNVVVGSDG-AEREVDAIIFGTGFHILDMPIGSK----VFDGDG 351
19              NVELIPHA---LAEVDGRVVVGADG-TRREVDVIIFGTGFDVSHPPIASR----IRGRDG 368
17              NVDLVTSG---ISEVTERGIRTDDG-TMHEADVIVYGTGFAAGDRFENEH----IVGRRG 356
5               KTVVITEG---IAEVRPHSIVAGDG-AERVVDAIIYATGFHVTDGFDNVE----LTGVGG 357
10              HVSLHRAS---FEKVTPEGVYTTEG-AFIPADVIILATGFKLQ-FTTSIE----IEGRDG 514
8               HVSLHRAS---PKHVHPGGVSLSSG-EFVEADVIVLATGFKVE-YASFID----ITGRNG 437
18              NVDLVDRS---VTAVRPEGLVDDQG-AENDVDVIVWATGFEAARFVSSMD----VVGMDG 520
HAPMO           NVSMIRQP---IEVITPKGICCVDG-TEHEFDLIVYGTGFHASKFLMPIN----VTGRDG 507
16              EVSIVTDH---IDTFTETGITLKSG-EELHADVVVTATGLNLLAFGGMT------LAVDG 374
EtaA            KVEVVTDT---IERFTATGIRLNSG-RELPADIIITATGLNLQLFGGAT------ATIDG 358
13              HASVVTDR---IERFTATGIRLESG-QELEADIVVTATGLNMLAFGAIQ------LSVDG 383
F               DGSIHLVSG-QVDHLTEDAVVLTDG-TELPADLVVYATGYGSMNGWAAD---------- 522
G               SGEVSVKQGTEIDHFTPDGVVFADG-TEMPVDVVVLATGYKNMRESARK---------- 529
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E               SGQVGLVQYADTAGFVAEGLSLTNG-DVVEADAVILATGYQTQQEGVRA----------- 518
D               RERGVLARQPMFGEITADGVRWPDG-RELKVDVILWCTGFRSSLDHLAP----------- 304
grogan          RARGVLAAVPPPARFSPTGMQWADG-TERAFDAVIWCTGFRPALSHLKG----------- 292
FMO1Ara         DKGMIRFKKSSKWWFYEEGIVFEDGT-TLEADVVILATGYDGKKKLKAIVPEPFRTWLEF 400
FMO2Ara         DKGMIRFKRTTNWWFYDEGIEFEDGT-TLEADVVILATGYDGMKKLKAIVPEPFRSWLEF 360
FMO1dog         LI------KPSIKEVKENSVVFNNTPKEEPIDIIVFATGYT---FAFPFLDET---VVKV 345
FMO1hum         FI------RPSIKEVKENSVIFNNTSKEEPIDIIVFATGYT---FAFPFLDES---VVKV 345
FMO2hum         KV------KSTVKELTETSAIFEDGTVEENIDVIIFATGYS---FSFPFLEDS---LVKV 345
FMO3hum         SV------KPNVKEFTETSAIFEDGTIFEGIDCVIFATGYS---FAYPFLDES---IIKS 345
FMO5hum         KV------KGNVKEFTETAAIFEDGSREDDIDAVIFATGYS---FDFPFLEDS---VKVV 346
FMO4hum         TM------KTSVIEFTETSAVFEDGTVEENIDVVIFTTGYT---FSFPFFEEP---LKSL 344
FMOFish         MV------KPNVQQIRGSSVVFEDGSVVDKVDVIVFATGYN---YDFPFLPPN---VMHK 346
FMO1Dro         QQ------KPDVRELDEKGAFFVDGS-YQEFDTVFFCTGYK---YAFPFLTVD-SGIYVE 276
FMO2Dro         TQ------KPDVKRFTKDGAVFTDGS-TESFDHVMFCTGYK---YTFPCLSTD-VGVQVI 284
FMOTyr          KR------KPDIKHFTPTGAVFVDGS-TEEFDVAILCTGYK---YSFPFLNYKSSGVAWT 334
H               GGKGWRTTLTHI----------DTGEIDSVGADIVVLATGYHFPLPEFLHT---------- 344
IucD_Lys        SGPGWKLLMEHH----------LDQGRESLESDVVIFATGYRSALPQILPS---------- 342
PVDA_Orn        QG----IELALR-------DAGSGELSVETYDAVILATGYERQLHRQLLE---------- 365
SidA_Orn        HGPQSRMRIHLKSSKPESEGAANDVKETLEVDALMVATGYNRNAHERLLS---------- 417
NRho_Orn        DG----IEVAVR-------SGVDGLTDTLACDALILATGFTPAPLEPLLG---------- 364
FMOMeth         QDQWYSFNMFDAQAWYARDVIMGRLPLPSKEEMKADSMAWREKELTLVT----------- 364
A               GVAPAIVDKELIAAIRDRSIEVVRGVESLDADSVWLVDGVRIDPEAMVC----------- 308
C               AAAGVEHFPAKVTGVHDGRPVLDDG-TAFDVRNVIWCTGFRKDTSWIQIP---------- 301
B               AGIDAPREERYVPVWRPEREVTELELPTSGITSVVWSIGFRTDYRWLHAG---------- 354
                                                  .

15              VPLSEYWSE--GPKTYLGLGVPGFPNLFVVTGPGSP-SVLANMVLGAEQHVDWIADCIEH 463
STMO            RTLKETWAA--GPRTYLGLGIDGFPNFFNLTGPGSP-SVLANMVLHSELHVDWVADAIAY 468
9               RNLRDEWSA--GPRTYLGLSVAGFPNMFILAGAGSP-SVLANMVLMAEQHVDWISNCLDY 454
14              LPLAEKWEH--GPRTYLGIMVNEFPNLFLITGPQSP-SVLYNMPLAIEDHVDFATDAIDY 457
PAMO            VALKEKWAA--GPRTYLGLSTAGFPNLFFIAGPGSP-SALSNMLVSIEQHVEWVTDHIAY 463
24              RKLQETWQD--GIRTYLGMMTTDFPNFFMVAGPQSP-ALASNVVMTIEQAVDWIADLIEH 469
CHMO            LAMKDYWKE--GPSSYMGVTVNNYPNMFMVLGPNGP---FTNLPPSIESQVEWISDTIQY 452
1               TLLRDKWSN--GVRANLGVATAGFPNLLFLYGPLSP-SGFCNGPSCAEIQGDLIVNTIDY 459
CPMO            QSFKDVWSD--GIRTQLGVATAGFPNLLFGYGPQSP-AGFCNGPSSAEYQGDLLIQLMNY 470
11              QLLSHKWSE--RLDTFMGLTTAGFPNLMFVYGPQSP-AGFCNGPTCAEVQGEIVVDFLTH 466
20              LSIQDKWKS--GVDTCMGLSTRGFPNMMFLYGPQSP-SGFCNGPTSAEYQGEIVVEFLQH 469
3               ETFEEVFRG--GSRTALGKATVGFPNLLYVYGPQSP-NAFCNGPTCAELEGEHLIQIVEH 463
4               VTLRDKWSQ--GVDAYLGAVTAGFPNAIFVYGPQSP-AAFANGSTNAELQGEVMVDFFEF 469
21              RALKDDWNR--DIRTTMGLMVHGYPNMLTTGAPLAPSAALCNMTTCLQQQTEWIAECIRY 467
23              RALKDDWNR--DIRTTMGLMVHGYPNMLTTGAPLAPSAALCNMTTCLQQQTEWIAECIRY 467
ACMO            RTLADDWSR--DIRTTMGLMVHGYPNMLTTAVPLAPSAALCNMTTCLQQQTEWISEAIRH 454
MEKMO           RSLKEQWQQ--EIRTAMGLQIHGYPNLFTTGAPLAPSAALCNMTTCLQQQVDWITGCIEF 470
CPDMO           QPLSDKWKD--GLSTLWGYHIRDFPN-CFILGNGQ-SAVTPNFTHMLNEAGKHVAYVVKH 514
CDMO            VKLSEHWAQ--GTRTLHGMHTYGFPN-LFVLQLMQGAALGSNIPHNFVEAARVVAAIVDH 520
7               RSLADVFDE-GGQQGYKGAAIANFPNMFFLVGPNTGLGHTSMVFMIES-QLNYLVDALQT 428
2               RTLAEHWD--GSPSAYKGTTVAGFPNLFLMYGPNTNLGHSSIVYMLES-QSAYIADALNV 413
12              RTLAEAWN--GNARAYLGTTISGFPNFFMLLGPNS-VVYTSQVVTIEA-QIAYILSCLQE 426
6               RSLDDHWK--GSPQAYLGTTVAGFPNAFVLLGPALGTGHTSAFMILEA-QLDYLIQAVTA 408
19              TLLSEKWS--KSPEAYLATTTPGAPNAYIMLGPNILV-YNSFLGLAET-QLDYVIDGLTT 424
17              LTIQRAWRD--GMEAYLGVAVAGFPNFFLMMGPNSGGGNQSIVFVIEA-QAHYITRCLAL 413
5               RRLADEWEE-HGIRTHLGITVAGYPNAFFLFGPNTGLGHNSVVFMIES-QIRYALELMDL 415
10              RTLSEVWNGGDDPRAYLGVQVAGFPNLFITAGPNSAPNHGAGHNILSEEHVHYIVECLQY 574
8               KKLADKWDHGQDPRAYLGIQVSGFPNLFVTAGPNAAPNHGAGHNITSEERVHYIVECLQY 497
18              RTLREVWND-DDPKAYLGVSVPGFPNFFMLGGPNSFPGSGS-FMFFMEVQMRYIRGLLTE 578
HAPMO           VALHDVWKG-DDARAYLGMTVPQFPNMFCMYGPNTGLVVYSTVIQFSEMTASYIVDAVRL 566
16              HDIDLTETM-----AYKGMMLSGVPNFAFVIGYTN-----ASWTLKADLVCEYVCRLLAH 424
EtaA            QQVDITTTM-----AYKGMMLSGIPNMAYTVGYTN-----ASWTLKADLVSEFVCRLLNY 408
13              EPVNPPDTT-----VYKSMMLSGLPNFVFALGYTN-----ISWTLKVDLISEHFCRLLDH 433
F               ----------------------------LMGQEVADKVGKCWGLGSDTTKDPGPWEGEQRN 555
G               ----------------------------FLGDAVADRCQDVWGLDA---------EGELRT 553
E               ---------------------------LLGDEIADAVGPIWGYDD---------EGEVRN 542
D               ----------------------------LRLRGPGGGITMTGRLATQVASD----PRIHLV 333
grogan          ----------------------------LDLVTPQGQVEVDG-SGLRALAV----PSVWLL 320
FMO1Ara         PSGVMPLYR-GTIHP--LIPNMGFVGYV-QSSSNLHTSELRSMWLSRLVDEKFRLPSKEK 456
FMO2Ara         PWGIMPLYR-GTIHP--LIPNMGFIGYV-QSSSNLKSSELHSRWLSQLLDGKFTLPSKEK 416
FMO1dog         ENGQASLYK-YIFPVHLPKPTLAVIGLIKPLGSMIPTGETQARWAVRVLKGINKLPPQSA 404
FMO1hum         EDGQASLYK-YIFPAHLQKPTLAIIGLIKPLGSMIPTGETQARWAVRVLKGVNKLPPPSV 404
FMO2hum         ENNMVSLYK-YIFPAHLDKSTLACIGLIQPLGSIFPTAELQARWVTRVFKGLCSLPSERT 404
FMO3hum         RNNEIILFK-GVFPPLLEKSTIAVIGFVQSLGAAIPTVDLQSRWAAQVIKGTCTLPSMED 404
FMO5hum         KN-KISLYK-KVFPPNLERPTLAIIGLIQPLGAIMPISELQGRWATQVFKGLKTLPSQSE 404
FMO4hum         CTKKIFLYK-QVFPLNLERATLAIIGLIGLKGSILSGTELQARWVTRVFKGLCKIPPSQK 403
FMOFish         SGHRLGLYK-HVFPPTLEHPTMAVVGFIHALGAIMPQAEMQSRWVTRVFKGHKKLPSNRA 405
FMO1Dro         DNYVQELYK-QCIN--IRNPSMALIGLP-FYVCAAQMMDIQARFIMSYYNGSNELPSTED 332
FMO2Dro         DNFVQPLWK-HCIN--INHPTMAFVGLP-FNVIPTHIFDMQVRFTLKFFTGQRKFPSREQ 340
FMOTyr          DKYVMPLYN-QLIN--INYPTMTFVGTG-KYSIG-LVRDRQGHYSAQLAAGLVKLPSQDE 389
H               ---------------------------LGGRIARTNCGLPQLAADYSVSWAGP---AGNKM 375
IucD_Lys        ---------------------------LMPLITMHDKNTFKVRDDFTLEWSGP---KENNI 373
PVDA_Orn        ---------------------------PLAEY--LGDHEIG--RDYRLQTDER---CKVAI 392
SidA_Orn        ---------------------------KVQHLRPTGQDQWKPHRDYRVEMDPSKVSSEAGI 451
NRho_Orn        ---------------------------DLAPK-IHPPREVG--RDYRLAVSPD---VTAGI 392
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FMOMeth          ----------AEEMYTYQGDYIQNLIDMTDYPSFDIPATNKTFLEWKHHKKENIMTFRD 413
A                ------------------------------ATGFRQELEKLVGHLGVLDERGWPHATGEKP 339
C                --------------------------VTGSDGWPEQSRGVSPDHPGLYFVGLPFLQAFAS 335
B                --------------------------VFDGEGHPTHNRGVTAVPGLYFLGLPWQHTWGSG 388


15               LWEKDYDAIEASVPATEQWVEHCRDLAAQTLFPLANSWYMGANIPGKPRVFMP-----YL 518
STMO             LDARGAAGIEGTPEAVADWVEECRNRAEASLLNSANSWYLGANIPGRPRVFMP-----FL 523
9                LDEHNIETIEATDESVDEWVAECNEKAAGTLFPTADSWYMGANIPGKPRVFMP-----YI 509
14               LDRRDLDVIEPTAQAESDWGALTNEIADQTLLPETNSWYMGANIPGKPRACMV-----YL 512
PAMO             MFKNGLTRSEAVLEKEDEWVEHVNEIADETLYPMTASWYTGANVPGKPRVFML-----YV 518
24               ARDSGATLVEATPEGQNDWVDITEETVAQTLYATTDSWYRGSNVEGKPNTFMG-----YV 524
CHMO             TVENNVESIEATKEAEEQWTQTCANIAEMTLFPKAQSWIFGANIPGKKNTVYF-----YL 507
1                MRDNGLNRIESEADADAAWSDHVAELTAEALYDKADSWYMGANVPGKPRQLLN-----YP 514
CPMO             LRDNNISRIEAQSEAQEEWSKLIADFWDSSLFPRAKSWYQGSNIPGKKVESLN-----FP 525
11               VRDGGYQRFETSEDAEQSWTAHVEEVFHMSLFPRAKSWYHGANIPGKPSQMLN-----YS 521
20               LRDNGITRFENTEESEKQWRAHVDELFVNSMFTKARSWYWGANVPGKPAQMLN-----YS 524
3                MRNNGYTRIEAKPEAQQYWGAHIAELTSATLFPLAKSWYMGANVPGKTVEMLM-----YP 518
4                LRSNGLTRFESTVEADKAWTAHINETDDTALFNRAKSWYNGGNIPGKKMQMLQ-----YL 524
21               MRAHDHTVIEPTLAGEDEWVAHHDETANATLVSKTDSWYNGANVPGKPRRVLS-----YI 522
23               MRAHDHTVIEPTRAGEDEWVAHHDETANATLVSKTDSWYNGANVPGKPRRVLS-----YI 522
ACMO             LRATGKTVIEPTAEGEEAWVAHHDELADANLISKTNSWYVGSNVPGKPRRVLS-----YV 509
MEKMO            AAEHGKHVVEASKALEDNWVQHHDETAAKTLVVKTDSWYMGSNVDGKPRRLLS-----YI 525
CPDMO            CLDERVDVFEPTAEAEQAWVDHVMSFAGIKQQYDRECTPSYYNNEGQVNDVALTRNNFYP 574
CDMO             VLSTGTSSVETTKEAEQAWVQLLLDHG--RPLGNPECTPGYYNNEGKPAELKDRLNVGYP 578
7                LDKYDIGKIEVRQDAQDRYNAELQEKLSHSVWNNGG--CASWYLDKHGNNTTL-----WP 481
2                MHHSEITAFEVTEEAQRRYNTRIQSELQTTVWNKGG--CSSWYYDSEGRNSVQ-----WP 466
12               MNAQGAASIDVRPEIQQAFVDEVDERLQTSVWNTGG--CNSYYLSGEGRNFTF-----YP 479
6                ARSNGWTRMEPRREVQDAFNAQVQEALATTVYNAGG--CQSYFLDVNGRNSFN-----WP 461
19               AERQGIEVLEVRDQPFRRFNDAVQKGLEPTVFNNGG--CSSYYLDADGRNFAA-----WP 477
17               MKKRDATRIEVRAGAQREFNRVVHRKLAGSVWNSGG--CDSWYLDSTGHNRAA-----WP 466
5                VDRRGADSAAVRPAVQSGFNADIQRKLARGVWSTGG--CVSWYLDSHGVNRTI-----WP 468
10               LLENGHDAMDVRQDVLDTYNRKVDAALDDTVWVHPGAEVNGYYRNSSGRAIVP-----CP 629
8                LVENDFSAMDVKPEALTVYNEKVDEALDQTVWAHPGEGVTGYYRNQQG---------- 545
18               MFKKGIKAIDARPEANEEYNELVDSTHARTVWTHRG--MSTYYRNSHGRVVFV-----MP 631
HAPMO            LLEGGHQSMEVKTPVFESYNQRVDEGNALRAWGFSK--VNSWYKNSKGRVTQN-----FP 619
16               MDANGFTQCAPER-DSSVEEEPFLDFAAGYVLRSVESFPKQGS-KAPWRLRMN-----YF 477
EtaA             MDDNGFDTVVVERPGSDVEERPFMEFTPGYVLRSLDELPKQGS-RTPWRLNQN-----YL 462
13               MDERGYTTVEPVLTDPGMERVPLLDLTSGYVQRAVAAFPRAGT-SGPWTAAMA-----YE 487
F                MWKPTQQEALWFHGGNLHQSRHYSLYLALQLKARHEEIPTPVYGLQEVHHLS-------- 607
G                VWRRSGHPGFWFMAGNLHQSRHYSKYLAFQIKAQEE-------GLQPIR---------- 595
E                TWRRTAQPGLWFSSGNFQLCRIYSKVLAMQIRTELDN------G---------------- 580
D                GYGPSSSTIGANRAG-QAAARELTRHLGLSAGSARPT---------------------- 369
grogan           GYGDWNGMASATLIGVTRYAREAVRQVTAYCADHQDR---------------------- 357
FMO1Ara          MLDQFLKEMEVTRNSSRFYKRHCISTFS--IQHADDMCNDMGLN----------PWRKSNF 505
FMO2Ara          MLDQFLKEMHVMRRSSRFFKNHCFSTFS--IQHADDLSKDMNLK----------P------ 459
FMO1dog          MTEEVNARKENKPSGFGLCYCKALQSD--YITYIDELLTNINAK--PNLFSLLLTDPRLA 460
FMO1hum          MIEEINARKENKPSWFGLCYCKALQSD--YITYIDELLTYINAK--PNLFSMLLTDPHLA 460
FMO2hum          MMMDIIKRNEKRIDLFGESQSQTLQTN--YVDYLDELALEIGAK--PDFCSLLFKDPKLA 460
FMO3hum          MMNDINEKMEKKRKWFG--KSETIQTD--YIVYMDELSSFIGAK--PNIPWLFLTDPKLA 458
FMO5hum          MMAEISKAQEEIDKRYVESQRHTIQGD--YIDTMEELADLVGVR--PNLLSLAFTDPKLA 460
FMO4hum          LMMEATEK-EQLIKRGVFKDTSKDKFD--YIAYMDDIAACIGTK--PSIPLLFLKDPRLA 458
FMOFish          MLKAVECDTKDMDKNYIVSKLVPLQVD--FVSYMDDIAGEVGVR--PSLAWLFFTDYPLF 461
FMO1Dro          MLKDTRDRMGKLWAEGLR-KRHAHMLGPKQIDYFTDLSQTAGVKNIKPVMTKLHNESSKC 391
FMO2Dro          MIADLEQEIGERWGCGVRNQKKAHQMGERQFVYYNELASIAGIENIKPVIHKLMKDCGKK 400
FMOTyr           MFKQWFDYTKHQTAKEINLIGYSNTES-----YMETLLNGTDIPRPPPVFTTILRNHIDI 444
H                FFLNAGKLSHGIADPNLSLASWRAATVLNTITETPLYPDLRSSTCSWDVADRAATHPPVD 435
IucD_Lys         FVVNASMQTHGIAEPQLSLMAWRSARILNRVMGRDLF-DLS--------------MPPA- 417
PVDA_Orn         YAQGFSQASHGLSDTLLSVLPVRAEEISGSLYQHLKPG-------------------TAA 433
SidA_Orn         WLQGCNERTHGLSDSLLSVLAVRGGEMVQSIFGEQLER-------------------AAV 492
NRho_Orn         YLQGGTEKTHGITSSLLSNVAVRAGEIVTSVVTRRGRNGTL----------------ASV 436
FMOMeth          HSYRSLMTGTMAPKHHTPWIDALDDSLEAYLSDKSEIPVAKEA---------------- 456
A                AAERLRFIGFVPRPSQIGFAAKQARRAARAIARELR------------------------ 375
C                MLTGGVGRDAAYVAKHIAKRVVVRSPEAVA---------------------------- 365
B                RFAGVARDAEYLADRIELEAGVLPATATLA---------------------------- 418


15               GGFGAYGRICADVAEEGFRG-FEFS-RSRTRLADPVG---------------------- 553
STMO             GGFGVYREIITEVAESGYKG-FAIL-EG------------------------------ 549
9                GGFGNYNTICAEVAAAGYKG-FELG-ERRVDVDQ------------------------- 541
14               GGAPTYRATCDEVVAGGYSG-FALT-RAEARAASTVS---------------------- 547
PAMO             GGFHRYRQICDEVAAKGYEG-FVLT---------------------------------- 542
24               GGVGKYRRMCTEIAKRGYPG-VRIDGETESPHLGPIHREIS------------------ 564
CHMO             GGLKEYRSALANCKNHAYEG-FDIQLQRSDIKQPANA---------------------- 543
1                GGLPLYLAKWDETVCAGYKG-FTLS---------------------------------- 538
CPMO             LGLPTYISKFNESAEKGYAG-FSLAS--------------------------------- 550
11               GGLPSYFDHWEENVAAGYKA-FTLS---------------------------------- 545
20               GGVPQYFARWDKIKANGYAA-FETN---------------------------------- 548
3                GGLSVYLEILEKAAAGGYQEQFELV---------------------------------- 543
4                NGVPTYLQFWQKEKESGYTDGLTVS---------------------------------- 549
21               GGVGTYREKTLAAAAAGYKG-FQLS---------------------------------- 546
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23              GGVGTYREKTLAAAAAGYKG-FQLS---------------------------------- 546
ACMO            GGVGAYRDATLEAAAAGYKG-FALS---------------------------------- 533
MEKMO           GGAGDYHRRCAEIAAQGYPG-FEMA---------------------------------- 549
CPDMO           GGAVAFINILREWREKGDFAQFQQRKR-------------------------------- 601
CDMO            AGSAAFFRMMDHWLAAGSFDGLTFR---------------------------------- 603
7               GFTFQFRNETKRFDLTAYDSV-ATADLPAPVHVNGKTPGPAAIPAQIDLDDDKVTAQ--- 537
2               TFTWKFRSQLQRFDQENYVSR-RRAAKETVA---------------------------- 496
12              GFNRRFRARTRRVDLHHYIISGAGASAKSIVRTAG------------------------- 514
6               WSTDRMRQRLGRFDEAAYDVS--REPAS----ATATSR--------------------- 493
19              WSTGSLRRRLARFDLENYAIRPYRTEQSPALHPSGKSR---------------------- 515
17              GSSASYWRRMRTPDDRHFELSSLAEREDDTEYRGPGVLTSGDLTVAVEVFLNGHIEPLDG 526
5               GSTVRYWQRTRSVEPADFEFT-------------PG------------------------ 491
10              WRLVDYWTMLREPNPDDLTFIGRRAEGRREASAR-------------------------- 663
8               ------------------------------------------------------------
18              FLNVEYWQMTRRPDLENYTAR-------------------------------------- 652
HAPMO           FTAVEFWQRTHSVEPTDYQLG-------------------------------------- 640
16              RDLVALRHGKILDDAMTFSRP-------------------------------------- 498
EtaA            RDIRLIRRGKIDDEGLRFAKRPAPVGV-------------------------------- 489
13              KDVERLREGPIEDADLRFTANQPALLAS------------------------------- 515
F               ------------------------------------------------------------
G               ------------------------------------------------------------
E               ------------------------------------------------------------
D               ------------------------------------------------------------
grogan          ------------------------------------------------------------
FMO1Ara         LLEAFSPYGSQDYRLGQEEKEDMTA---------------------------------- 530
FMO2Ara         ------------------------------------------------------------
FMO1dog         LTIFFGPCTPYQFRLTGPGKWKGARNAILTQWDRTFKVTKTRIVQ--ESPTPFASLLKLL 518
FMO1hum         LTVFFGPCSPYQFRLTGPGKWEGARNAIMTQWDRTFKVIKARVVQ--ESPSPFESFLKVF 518
FMO2hum         VRLYFGPCNSY------------------------------------------------ 471
FMO3hum         MEVYFGPCSPYQFRLVGPGQWPGARNAILTQWDRSLKPMQTRVVGRLQKPCFFFHWLKLF 518
FMO5hum         LHLLLGPCTPIHYRVQGPGKWDGARKAILTTDDRIRKPLMTRVVERSSSMTSTMTIGKFM 520
FMO4hum         WEVFFGPCTPYQYRLMGPGKWDGARNAILTQWDRTLKPLKTRIVPDSSKPASMSHYLKAW 518
FMOFish         KRVLWGPVTAYQYRITGPGKWSGARRAIFTQFERMFQPFKTRQVEEKQGCSVAGRLLKLS 521
FMO1Dro         FNENLLHFREDNFAILDDETFIKLN---------------------------------- 416
FMO2Dro         YIFELDTYRSNKYTILDDENFLKNGEAIV------------------------------ 429
FMOTyr          WYTEFLTFRNYQINLLSDTEYEMIYKPQKKVCPLDVQV--------------------- 482
H               SGVDLLTESSRQ---------------------------------------------- 447
IucD_Lys        ----LIQWRSGT---------------------------------------------- 425
PVDA_Orn        RALHEHALAS------------------------------------------------ 443
SidA_Orn        QGHQLRAML-------------------------------------------------- 501
NRho_Orn        NAQDTYATSEAR---------------------------------------------- 448
FMOMeth         ------------------------------------------------------------
A               ------------------------------------------------------------
C               ------------------------------------------------------------
B               ------------------------------------------------------------


15              ------------------------------------------------------------
STMO            ------------------------------------------------------------
9               ------------------------------------------------------------
14              ------------------------------------------------------------
PAMO            ------------------------------------------------------------
24              ------------------------------------------------------------
CHMO            ------------------------------------------------------------
1               ------------------------------------------------------------
CPMO            ------------------------------------------------------------
11              ------------------------------------------------------------
20              ------------------------------------------------------------
3               ------------------------------------------------------------
4               ------------------------------------------------------------
21              ------------------------------------------------------------
23              ------------------------------------------------------------
ACMO            ------------------------------------------------------------
MEKMO           ------------------------------------------------------------
CPDMO           ------------------------------------------------------------
CDMO            ------------------------------------------------------------
7               ------------------------------------------------------------
2               ------------------------------------------------------------
12              ------------------------------------------------------------
6               ------------------------------------------------------------
19              ------------------------------------------------------------
17              LYHWYGRVVGDGVDAAKGRNRTPLFLTIGDGPEVPAALAERDPWGHFRIAGVGTPPFPLA 586
5               ------------------------------------------------------------
10              ------------------------------------------------------------
8               ------------------------------------------------------------
18              ------------------------------------------------------------
HAPMO           ------------------------------------------------------------
16              ------------------------------------------------------------
EtaA            ------------------------------------------------------------
13              ------------------------------------------------------------
F               ------------------------------------------------------------
```

```
G               ------------------------------------------------------------
E               ------------------------------------------------------------
D               ------------------------------------------------------------
grogan          ------------------------------------------------------------
FMO1Ara         ------------------------------------------------------------
FMO2Ara         ------------------------------------------------------------
FMO1dog         SLLALLMAIFLIFL------------------------------------------- 532
FMO1hum         SFLALLVAIFLIFL------------------------------------------- 532
FMO2hum         ------------------------------------------------------------
FMO3hum         AIPILLIAVFLVLT------------------------------------------- 532
FMO5hum         LALAFFAIIIAYF-------------------------------------------- 533
FMO4hum         GAPVLLASLLLICKSSLFLKLVRDKLQDRMSPYLVSLWRG----------------- 558
FMOFish         LTAMVGGAAAYYFHLQPPSSLT--YLLSKLTPQRV--------------------- 554
FMO1Dro         ------------------------------------------------------------
FMO2Dro         ------------------------------------------------------------
FMOTyr          ------------------------------------------------------------
H               ------------------------------------------------------------
IucD_Lys        ------------------------------------------------------------
PVDA_Orn        ------------------------------------------------------------
SidA_Orn        ------------------------------------------------------------
NRho_Orn        ------------------------------------------------------------
FMOMeth         ------------------------------------------------------------
A               ------------------------------------------------------------
C               ------------------------------------------------------------
B               ------------------------------------------------------------


15              ----------------
STMO            ----------------
9               ----------------
14              ----------------
PAMO            ----------------
24              ----------------
CHMO            ----------------
1               ----------------
CPMO            ----------------
11              ----------------
20              ----------------
3               ----------------
4               ----------------
21              ----------------
23              ----------------
ACMO            ----------------
MEKMO           ----------------
CPDMO           ----------------
CDMO            ----------------
7               ----------------
2               ----------------
12              ----------------
6               ----------------
19              ----------------
17              PVEVEVPISRAKLASAE 603
5               ----------------
10              ----------------
8               ----------------
18              ----------------
HAPMO           ----------------
16              ----------------
EtaA            ----------------
13              ----------------
F               ----------------
G               ----------------
E               ----------------
D               ----------------
grogan          ----------------
FMO1Ara         ----------------
FMO2Ara         ----------------
FMO1dog         ----------------
FMO1hum         ----------------
FMO2hum         ----------------
FMO3hum         ----------------
FMO5hum         ----------------
FMO4hum         ----------------
FMOFish         ----------------
FMO1Dro         ----------------
FMO2Dro         ----------------
FMOTyr          ----------------
H               ----------------
IucD_Lys        ----------------
PVDA_Orn        ----------------
SidA_Orn        ----------------
```

NRho_Orn ----------
FMOMeth ----------
A ----------
C ----------
B ----------

Sequences used in tree and alignment

Newly cloned *Rhodococcus jostii* RHA1 type II FMO & NMO-H

>a
MSEHQVAIVGAGTSGVAAAVALADRGINPLLIDRADQVGSSWHSRYDRLRLNTGRQFSHLPNRPYPKGTP
TFPTREQVIEHLERHARADGIELRLGCPVERLDLTDGHWRLTTAAGSVDAAEVVVATGFDHEPFVPDWPG
RGDWRGALVHSSQYRNPSQYNGKRVLVVGAGCSGMEIAYDLATGGAAKVWLSARTPPNIMLRQGPGGIPG
DFIATPLYHAPVPIADAIARFGRERSIGDLREFGLPIPDEGIFARSARLGVAPAIVDKELIAAIRDRSIE
VVRGVESLDADSVWLVDGVRIDPEAMVCATGFRQELEKLVGHLGVLDERGWPHATGEKPAAERLRFIGFV
PRPSQIGFAAKQARRAARAIARELR

>b
MTEQHTVVVIGGGQAGLSISWHLVQRGIDHVVLERESIAHEWRDSRWDSFTLVTPNWQCTLPGYTYSGGD
PDGFMNREQTYQFVRGYADTFDPPVREGVAVVAVRQSGSGGFDVDTTEGPMHADHVVVAVGGYHTPVVPR
FAERLPADITQLHSSQYRSAGALPAGEVLVVGNGQSGAQIAEDLHLAGRTVHLVTGGAPRVARFYRGRDC
VAWLHDMGTYDVSIADHPGGLGKRENTNHYVTGRDGGRDIDLRAFALAGMRLYGRLLDVVDGTLRFAPTL
ESSLDAADAVSESIKDSIDAYIDRAGIDAPREERYVPVWRPEREVTELELPTSGITSVVWSIGFRTDYRW
LHAGVFDGEGHPTHNRGVTAVPGLYFLGLPWQHTWGSGRFAGVARDAEYLADRIELEAGVLPATATLA

>c
MSTERFETIVIGAGQAGLATGYHLTRCGQRFVILDAHDRVGDVWRERFDSLRLYSPARYDGLPGWGIPAP
AWSWPGKDEVADYFEAYAQRFALPIRTGTTVDGLSRDGDRYVVTAGTDRFEADNVVVASGTWQSPVVPDL
AERLDPRIRQLHSSDYRNPSQLQDGPVLVVGCSHSGADIALEASRSHRTTICGPVRGEVPFDIEGRLAHL
AVPIMWFMANHVLTERTPVGRKMCTHVRSGGGPLLRVKRADLAAAGVEHFPAKVTGVHDGRPVLDDGTAF
DVRNVIWCTGFRKDTSWIQIPVTGSDGWPEQSRGVSPDHPGLYFVGLPFLQAFASMLTGGVGRDAAYVAK
HIAKRVVVRSPEAVA

>d
MNSEVDVAVIGAGQAGLSAAYYLRRFGVEPESGFVVLDHAPGPGGAWQFRWPSLTLSTVNGVHDLPGLGF
ADTIGVDPNDPEAALVHAASAVPQYFATYEKQFELPVHRPVHTRVVCARDERLRIETDRGVVSARGLINA
TGTWERPFIPRYPGAESFTGRQVHTKDYSSAQDFAGQHVLVVGGGISAVQLLDEISRVTTTTWVTRRPPE
FRDEPFTPEIGRAAVALVEDRVRRGLPPGSVVSVTGLPVTPAIRAARERGVLARQPMFGEITADGVRWPD
GRELKVDVILWCTGFRSSLDHLAPLRLRGPGGGITMTGRLATQVASDPRIHLVGYGPSSSTIGANRAGQA
AARELTRHLGLSAGSARPT

>e
MTTTFSDTDLRTDAQAWLDGFSRFLAAELAPTAVFAPQAYWRDVLAFTGDLRTFSDEIPAELLRRQELTK
ATNIRIAEDRTPPRLVERAGIPCLEVIFEFDTLAGSAVGVARLVDVPERGLLVRSLFTTLDQLADHPERT
GEHRPVGQADSSKFGGPNWLDRRIAAQAYENRDPDVLIVGGGQSGLTLAARLGQLDVDALVVDTHARPGD
NWRTRYHALTLHNAVWLNDLPYMPFPATWPQFVPKDKLAGWFEAYVEAMEINFWGTTAFIGGDYDEQSQS
WVARVRRGDGTVRTLRPKHVVIATGVSGIPYVPELPGLSQFAGRTLHSSEYDDANDFAGQRVVIIGTGNS
AHDVAQDLHAHGIDVTMVQRSSTTIVSVDPSAAAADASYLTAPTLEDCDLLSMATVYPDLYTGSQMITAT
MKELDKDLVAALNRIGFRTDYGEEDTGQQMKFMRRGGGYYLNVGCSDLLISGQVGLVQYADTAGFVAEGL
SLTNGDVVEADAVILATGYQTQQEGVRALLGDEIADAVGPIWGYDDEGEVRNTWRRTAQPGLWFSSGNFQ
LCRIYSKVLAMQIRTELDNG

>f
MTQTVQPAAVQTSLTPQERVDLWLASFESALAARDVDRAAGMFAVDSFWRDLVAFTWNLKTVEGRDAVAA
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NRVKGAVHGSGGDTLSWAEKREIEERELGYTRQPYVLVIGGGQGGIALGARLRQLGVPAIVVDKNERPGD
QWRNRYKSLCLHDPVWYDHLPYMPFPDNWPVFAPKDKIGDWLEMYTKVMEIPYWSSTTCTSATFDDETKE
WTVVLDRDGEDVVLHPKQLVLATGMSGKPNVPSFPGQDVFRGEQHHSSRHPGPDAYVGKRVVVVGANNSA
HDICKALFENGADVTMLQRSSTHIVKSDSLMDLGLGDLYSERAVAAGMTTEKADLTFASLPYKIMHEFQI
PIYQKIAERDRDFYDRLEKAGFKLDFGDDGSGLFMKYLRRGSGYYIDVGASELVADGSIHLVSGQVDHLT

EDAVVLTDGTELPADLVVYATGYGSMNGWAADLMGQEVADKVGKCWGLGSDTTKDPGPWEGEQRNMWKPT
QQEALWFHGGNLHQSRHYSLYLALQLKARHEEIPTPVYGLQEVHHLS

>g
MTATLDAPVDTNIPQPGDIARRWLAGFGATLERGDARGAAQHFLVDGWWRDLLSFTWDLHTTHGRADIES
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EIKGHEEKKGHRRVQGTNHGAHRGKINWLDRRTAKGEFETEQPAVVIVGAGQGGLALAARLGQLGVDTLL
VERNDRIGDSWRKRYHSLVLHDPVWYDHLPYLNFPDHWPVFTPKDKLANWFEFYADAMELNVWTGTEFTG
GSYDDATGEWTVTVARDDGSTRTLHPRHVVLATGMSGVPNIPRIAGADTFEGTIEHSSWFVGGREMQGKK
ALVVGCCNSGHDIAQELNEQGADVTILQRSSTYVMSSKHGIPGLFGGVYEEGGPAVQDADLIFASLPYPL
LAGIHAGATEAIAEKDAEMLDGLRKAGFKVDFGEDGSGLFMKYLRRGGGYYIDVGASELIASGEVSVKQG
TEIDHFTPDGVVFADGTEMPVDVVVLATGYKNMRESARKFLGDAVADRCQDVWGLDAEGELRTVWRRSGH
PGFWFMAGNLHQSRHYSKYLAFQIKAQEEGLQPIR

>hNMO
MLEHLDLVGIGAGPSNLSVAALSAPVGRLRCKFLDRQPTQRWYPGLMLSAAVLQVSHLKDLVTLVDPTSR
YTFLNFLARTGRLHRFASLHTPLIARREYESYLRWVSDQLDEVQFGCAVEEVTFDGQAFRVESTRGTYAA
QHLSIGVGPRPYVPELATGTLGEDVFHSSDFGYHTDSLAGRDVVVVGGGQSGAEVVEHLLQRSGRDAVGS
LTWASRRIGFQPLDESPFTNEWFHPDYVRYFHGLSQSRRSQLLDAQQLASDGISKGLLESIYRRLYYNDF
VDSDRIRTTLLPGRELTGLCRGPGGKGWRTTLTHIDTGEIDSVGADIVVLATGYHFPLPEFLHTLGGRIA
RTNCGLPQLAADYSVSWAGPAGNKMFFLNAGKLSHGIADPNLSLASWRAATVLNTITETPLYPDLRSSTC
SWDVADRAATHPPVDSGVDLLTESSRQ

>X (FMO Grogan)
MDSVDVVVIGGGQSGLSAGYFLRRSGLSYVILDAEASPGGAWQHAWHSLHLFSPAGWSSIPGWPMPASQGPYPARAEVLAYLAQYEQKY
ALPVLRPIRVQRVSHFGERLRVVARDGRQWLARAVISATGTWGEAYTPEYQGLESFAGIQLHSAHYSTPAPFAGMRVAIIGGGNSGAQI
LAEVSTVAETTWITQHEPAFLADDVDGRVLFERATERWKAQQEGREPDLPPGGFGDIVMVPPVLDARARGVLAAVPPPARFSPTGMQWA
DGTERAFDAVIWCTGFRPALSHLKGLDLVTPQGQVEVDGSGLRALAVPSVWLLGYGDWNGMASATLIGVTRYAREAVRQVTAYCADHQD
R

Rhodococcus jostii RHA1 type II BVMO:

>9
MTVQDNDFDAVVVGAGISGLYAVYKLRQRGMRVHGFESAEGVGGTWYHNRYPGARCDVESIDYSYSFDEELQQEWTWTERFATQDEILR
YLEHVADRHDLRSAYDFLTRVTSATYDEETTRWSITTDTGQNVTARFCVLATGVLSATNKPDIPGRDTFGGATYHTGEWPHEPVDFAGK
RVGVIGTGSSGIQSIPVIAEEAAEVFVFQRSPNYSIPAGNRPLTGEYIAEVKANYAERRRLSRMSGGGTPNSAYPKGALEVDAEERRRV
YDEWWQRGGYLFAKAFPDQTISQAANDTAREYVEAKIREMVTDPDIADQLVPTDHPIGTKRIVTDNGYFKTFNRGNVTLVNLRRTPITE
ITEAGVLTTNSFYGLDMLVFATGFDAMTGSLSRIDIRGRAGRNLRDEWSAGPRTYLGLSVAGFPNMFILAGAGSPSVLANMVLMAEQHV
DWISNCLDYLDEHNIETIEATDESVDEWVAECNEKAAGTLFPTADSWYMGANIPGKPRVFMPYIGGFGNYNTICAEVAAAGYKGFELGE
RRVDVDQ
>15
MSARTEVDARANRIGDVDAVVVGAGFAGLYAVHKLRSLGLTVQGVEAAGGVGGTWFWNRYPGARCDVESVDYSYSFSRELEQEWDWSEK
YATQPEILAYINHVADRFDLRDRFLFGTRVTSAELDEESLRWEVRTDRGDVLSARYCIFATGALSTANMPNIAGRESFTGDTHHTGQWP
HEGVDFTGRRVGIIGTGSSGIQSIPLIAEQAEHLYVFQRSANYSVPAGNQAWDDEMRRAIKAGYEERRRLSRESGGGSPYNAHPKSALD
VSDEERREAYETRWKLGGVLFAKTFPDQTKTEAANATAREFAEEKIRLLVDDPAVADKLIPNDHPIGTKRIVTDTHYFETYNRPNVTLV
DLKAAPIESITPSGITTADADYALDTLVFATGFDAMTGALDRMRIVGRGGVPLSEYWSEGPKTYLGLGVPGFPNLFVVTGPGSPSVLAN
MVLGAEQHVDWIADCIEHLWEKDYDAIEASVPATEQWVEHCRDLAAQTLFPLANSWYMGANIPGKPRVFMPYLGGFGAYGRICADVAEE
GFRGFEFSRSRTRLADPVG
>14
MSKTISADVDVVVVGAGFAGLYALRKLRDTMKLSTRVFEAGSEVGGTWFWNRYPGARCDIESVHYSYSFDEDLQQEWQWSERFAGQPEI
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GKRVAVIGTGASGIQAIPFIAEDAAELVVFQRTPNFATPLGNGPMDPNELADIKSNYADVRTAARNHFLGVPFNQVQPSALAVDAEERR
RTFDERWNAGGFRLFIDSYQDILFDKKANDTIADYIRDRIHERVQDPAKAATLAPTGYAYGTKRPPLETNYYEAFNRDSVSVVDVKSTP
IDEITPTGVRVGDRVYEVDTIVLATGFDAMTGPLMAMDIRGRGGLPLAEKWEHGPRTYLGIMVNEFPNLFLITGPQSPSVLYNMPLAIE
DHVDFATDAIDYLDRRDLDVIEPTAQAESDWGALTNEIADQTLLPETNSWYMGANIPGKPRACMVYLGGAPTYRATCDEVVAGGYSGFA
LTRAEARAASTVS
>24
MTTSMKAANPMNFPSTSDTGIVDVLGVGAGFSGLYLSHRLTTAGWTFAGFEAGPSVGGTWFWNTYPGARCDVESIYYSYSFDEALQQEW
TWSQRFAPQAEILSYINHVADRFDLRKHFTFNTRVVGATWNAAERLWEVQLDNGETRRGRYLISGAGGLSTPKDFDVPGLGNFTGLQVS
TSRWNISLDDLAGKRVAVIGTGSSGVQAIPLIAEVAEHVTVFQRTPNYVMPARNAELPLERVDSIKDDYPAIREECRHSPGGIPDRPVT
DKAFDVSAEERQRRYEAAYERSGFNGVGGEFADLLTDVEANRTASEFIHDKIREIVEDPATAELLVPRYHPLGAKRSVFGTDYYETYNR
PNVSLVSLRDEPIETMTANAIVTSKGTYEADAVVLAIGFDAFTGPLYGLGLTGASGRKLQETWQDGIRTYLGMMTTDFPNFFMVAGPQS

PALASNVVMTIEQAVDWIADLIEHARDSGATLVEATPEGQNDWVDITEETVAQTLYATTDSWYRGSNVEGKPNTFMGYVGGVGKYRRMC
TEIAKRGYPGVRIDGETESPHLGPIHREIS
>1
MSTAAPAVTEVLDVLVVGAGFAGLYQLENLRSRGYSVKVVEAGEGLGGIWHWNRYPGARVDSEGPIYQFTRPDLWDEFAFSELYPGGDE
LRRYFKYVDAKLDLSKDIYYNTRIISAEFDDTANTWTVTAENGSSFVCKYFVLCTGFAAKPIFPKLPGMDSFTGINHHTGLWPEGGIEF
AGKRIAIIGTGASGVQVAQEASKKAAQLTVFQRTPVQALPMRQRQLTDEDNAKIKFDLADRFSRRSASFSGFDFDFIPKSALGVSDEER
ITTYERLWECGFEFWLGTYQDVFVDDDANDTAYEFWRDRTRARIKDPVIAEKLAPTKKAYPFGVKRPSLEQTYYDIFNQDNVRVVDLHE
DPIETITPTGLKTTSEQHEFDIIVYATGFDAVTGGLTAMDIRGTDGTLLRDKWSNGVRANLGVATAGFPNLLFLYGPLSPSGFCNGPSC
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FTLS
>11
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DIVDVNEDPIERITPAGVQTKSGLHEFDILVFATGFDANRGGITSIDIRGTNDQLLSHKWSERLDTFMGLTTAGFPNLMFVYGPQSPAG
FCNGPTCAEVQGEIVVDFLTHVRDGGYQRFETSEDAEQSWTAHVEEVFHMSLFPRAKSWYHGANIPGKPSQMLNYSGGLPSYFDHWEEN
VAAGYKAFTLS
>20
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RWPQEGVDMTGRKVVVMGTGSSGVQVVQEAGHVAEHVTVFQRTPNLAIPMQQRALTHDDNEQFRKGLPERFEARYKAFAGFDFDFLPQN
AADLSMEERDAIYEKMWAEGGFEMWLGNFQDILVDEDANRTFYDFWRNKVLERVTDPKKAAIVAPETPPHPYGVKRPSLEQDYFDVINQ
SNVEVIDSNLTPIRRVLPHGIETDDGVIECDLLVLATGFDNNSGGIMAIDITGVDGLSIQDKWKSGVDTCMGLSTRGFPNMMFLYGPQS
PSGFCNGPTSAEYQGEIVVEFLQHLRDNGITRFENTEESEKQWRAHVDELFVNSMFTKARSWYWGANVPGKPAQMLNYSGGVPQYFARW
DKIKANGYAAFETN
>4
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WRSDLDMTGKRVAIIGTGASAVQVVQEAGPVVENLTVFQRTPNISLPMQQKYLDDEEQAALKNKMPDVAAKCRETHAAIDYDFDPRSGF
ETPEDERNAVFERLWNQGGFAFWLGNFSDYLFNDKTNALTYEFWKNKIKPQIKDPVKAELLVPEIAPHPFGAKRPALHQNYYEVMNQTN
VSLVSTKETPIVGFTETGIRTADGVEHGEFDIIVLATGFNNNTGALTSIDVQNANGVTLRDKWSQGVDAYLGAVTAGFPNAIFVYGPQS
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QKEKESGYTDGLTVS
>7
MVSYMSLPVTDTSAPPAGVRHIDTLIIGSGFAGLGAAIKLTQAGKTDFLVLERGSDVGGTWRDNTYPGAACDVPSHLYSYSFALNPEWT
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NHDADLTGKRVAVIGTGASAIQIVPAIGKKVSHLDVYQRTAPWILPRADREYTKLEHTAFKYLPGFQKLCRTGIYWMRESQVVGLAKAP
VFMKPLQFAAERHLRRQIKDKALRKKVTPNFQIGCKRMLISNNYYPTLAQDNVDLVTDGIAEVTADSVVSKDGTVREVDAIVVATGFHV
TDSPTFEGIFGKDGRSLADVFDEGGQQGYKGAAIANFPNMFFLVGPNTGLGHTSMVFMIESQLNYLVDALQTLDKYDIGKIEVRQDAQD
RYNAELQEKLSHSVWNNGGCASWYLDKHGNNTTLWPGFTFQFRNETKRFDLTAYDSVATADLPAPVHVNGKTPGPAAIPAQIDLDDDKV
TAQ
>10
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EREDVGGTWYRNTYPGAAVDTPSHYYSYSFELNPNWSKYYPTGPEYQNYLLDVVEKYRLREHIRFRTRVLSARWLDDEHRWEVVTEDGE
GSVVRHRARAVITAMGMLNAANIPEVDGLDSFAGRVVHTAEWDSDLDLSGKRVVVLGTGCTSVQVVANIVDQVEALDVVVRSPHWLVPE
KAVSGDVTEGEKWALANLPFYDRWFRLRSYWFASDNLYPLPRIDKEWAATHLSASPANDMVLRTAQEYLQTSFTDRPDLIAKLTPDFRP
YAKRIVKDPGFFAALNREHVSLHRASFEKVTPEGVYTTEGAFIPADVIILATGFKLQFTTSIEIEGRDGRTLSEVWNGGDDPRAYLGVQ
VAGFPNLFITAGPNSAPNHGAGHNILSEEHVHYIVECLQYLLENGHDAMDVRQDVLDTYNRKVDAALDDTVWVHPGAEVNGYYRNSSGR
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>2
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GTGASAVQFVPEIAPVAEHLTVFQRTPAWVIPRLDRELSGSEKRLYRRLPLVQKAVRGTVYGFREALGGVLAHATGLLPVFEMVAKAHL
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>17
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VGTGASAVQFVPEVAKTAAHVDVFQRTPHWILPKLDRPITAGEKAVFKAVPGVQKAYRGAIYWSHESLIAGFLHPRLMTVLESAARGLL
RRQVRDPELRATLTPDYIIGCKRILVSSNFYPALQRGNVDLVTSGISEVTERGIRTDDGTMHEADVIVYGTGFAAGDRFENEHIVGRRG
LTIQRAWRDGMEAYLGVAVAGFPNFFLMMGPNSGGGNQSIVFVIEAQAHYITRCLALMKKRDATRIEVRAGAQREFNRVVHRKLAGSVW
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>18
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Type II BVMO

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Type I FMO

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